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(54) Title: CELL CYCLE PROGRESSION PROTEINS

(57) Abstract: Polynucleotides encoding a number of *Drosophila* gene products are provided. Polynucleotide probes derived from these nucleotide sequences, polypeptides encoded by the polynucleotides and antibodies that bind to the polypeptides are also provided.

## CELL CYCLE PROGRESSION PROTEINS

The present invention relates to a number of genes implicated in the processes of cell cycle progression, including mitosis and meiosis.

We have now identified a large number of genes in *Drosophila*, mutations in  
5 which disrupt cell cycle progression, for example the processes of mitosis and/or meiosis. We have determined the phenotypes of these mutations and recovered nucleotide sequences associated with the corresponding genes. Many of these nucleotide sequences correspond to protein open reading frames (ORFs) present in the *Drosophila* genome.

Accordingly the present invention provides in one aspect a polynucleotide selected  
10 from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or  
15 a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

There is provided, according to another aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof; (b) polynucleotides  
20 comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined  
25 in (a), (b) or (c).

We provide, according to yet a further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide

sequences set out in Examples 15 to 19 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in  
5 Examples 15 to 19 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

As a further aspect of the present invention, there is provided a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out  
10 in Examples 20 to 30 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence  
15 which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

We provide, according to a yet further aspect of the present invention, a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof; (b) polynucleotides  
20 comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof; (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a),  
25 (b) or (c).

The present invention, in a further aspect, provides a polynucleotide selected from: (a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof; (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof; (c)

polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof; (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).

- 5           A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of the above aspects of the invention.

          The present invention also provides a polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a  
10   homologue, variant, derivative or fragment thereof.

          Preferably the polypeptide is encoded by a cDNA sequence obtainable from a eukaryotic cDNA library, preferably a metazoan cDNA library (such as insect or mammalian) said DNA sequence comprising a DNA sequence being selectively detectable with a *Drosophila* nucleotide sequence as shown in any one of Examples 1 to 70.

- 15           The term "selectively detectable" means that the cDNA used as a probe is used under conditions where a target cDNA of the invention is found to hybridize to the probe at a level significantly above background. The background hybridization may occur because of other cDNAs present in the cDNA library. In this event background implies a level of signal generated by interaction between the probe and a non-specific cDNA  
20   member of the library which is less than 10 fold, preferably less than 100 fold as intense as the specific interaction observed with the target cDNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with <sup>32</sup>P. Suitable conditions may be found by reference to the Examples, as well as in the detailed description below.

          A polynucleotide encoding a polypeptide of the invention is also provided.

- 25           The present invention further provides a vector comprising a polynucleotide of the invention, for example an expression vector comprising a polynucleotide of the invention



operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.

Also provided is an antibody capable of binding a polypeptide of the invention.

5 In a further aspect the present invention provides a method for detecting the presence or absence of a polynucleotide of the invention in a biological sample which method comprises: (a) bringing the biological sample containing DNA or RNA into contact with a probe comprising a nucleotide of the invention under hybridising conditions; and (b) detecting any duplex formed between the probe and nucleic acid in the sample.

10 In another aspect the invention provides a method for detecting a polypeptide of the invention present in a biological sample which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

15 Knowledge of the genes involved in cell cycle progression allows the development of therapeutic agents for the treatment of medical conditions associated with aberrant cell cycle progression. Accordingly, the present invention provides a polynucleotide of the invention for use in therapy. The present invention also provides a polypeptide of the invention for use in therapy. The present invention further provides an antibody of the  
20 invention for use in therapy.

In a specific embodiment, the present invention provides a method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of a polynucleotide, polypeptide and/or antibody of the invention.

25 The present invention also provides the use of a polypeptide of the invention in a method of identifying a substance capable of affecting the function of the corresponding

gene. For example, in one embodiment the present invention provides the use of a polypeptide of the invention in an assay for identifying a substance capable of inhibiting cell cycle progression. The substance may inhibit any of the steps or stages in the cell cycle, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, and cytokinesis functions. For example, possible functions of genes of the invention for which it may be desired to identify substances which affect such functions include chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation, microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In a further aspect the present invention provides a method for identifying a substance capable of binding to a polypeptide of the invention, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.

In an additional aspect, the invention provides kits comprising polynucleotides, polypeptides or antibodies of the invention and methods of using such kits in diagnosing the presence of absence of polynucleotides and polypeptides of the invention including deleterious mutant forms.

Also provided is a substance identified by the above methods of the invention. Such substances may be used in a method of therapy, such as in a method of affecting cell cycle progression, for example mitosis and/or meiosis.

The invention also provides a process comprising the steps of: (a) performing one of the above methods; and (b) preparing a quantity of those one or more substances identified as being capable of binding to a polypeptide of the invention.

Also provided is a process comprising the steps of: (a) performing one of the above  
5 methods; and (b) preparing a pharmaceutical composition comprising one or more substances identified as being capable of binding to a polypeptide of the invention.

We further provide a method for identifying a substance capable of modulating the function of a polypeptide of the invention or a polypeptide encoded by a polynucleotide of the invention, the method comprising the steps of: incubating the polypeptide with a  
10 candidate substance and determining whether activity of the polypeptide is thereby modulated.

A substance identified by a method or assay according to any of the above methods or processes is also provided, as is the use of such a substance in a method of inhibiting the function of a polypeptide. Use of such a substance in a method of regulating a cell  
15 division cycle function is also provided.

#### **DETAILED DESCRIPTION OF THE INVENTION**

The practice of the present invention will employ, unless otherwise indicated, conventional techniques of chemistry, molecular biology, microbiology, recombinant DNA and immunology, which are within the capabilities of a person of ordinary skill in  
20 the art. Such techniques are explained in the literature. See, for example, J. Sambrook, E. F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Second Edition, Books 1-3, Cold Spring Harbor Laboratory Press; Ausubel, F. M. et al. (1995 and periodic supplements; *Current Protocols in Molecular Biology*, ch. 9, 13, and 16, John Wiley & Sons, New York, N.Y.); B. Roe, J. Crabtree, and A. Kahn, 1996, *DNA Isolation and Sequencing: Essential Techniques*, John Wiley & Sons; J. M. Polak and James O'D.  
25 McGee, 1990, *In Situ Hybridization: Principles and Practice*, Oxford University Press; M. J. Gait (Editor), 1984, *Oligonucleotide Synthesis: A Practical Approach*, Irl Press; and, D.

M. J. Lilley and J. E. Dahlberg, 1992, *Methods of Enzymology: DNA Structure Part A: Synthesis and Physical Analysis of DNA* Methods in Enzymology, Academic Press. Each of these general texts is herein incorporated by reference.

Preferably, the polypeptides and polynucleotides of the invention are such that they  
 5 give rise to or are associated with defined phenotypes when mutated.

For example, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to complete cytokinesis; such polypeptides and polynucleotides are conveniently categorised as "Category 1". Phenotypes associated with Category 1 polypeptides and polynucleotides include any one or more of the following,  
 10 singly or in combination: Mitotic defects in brain: cytokinesis defect (polyploidy); Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects.(Seg-01/62); Meiotic defects in testis: cytokinesis defects, abnormal spindles.(Ab-02/12); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, high polyploidy); Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant; Meiotic  
 15 defects in testis: cytokinesis defects; Meiotic defects in testis:segregation defect, cytokinesis defect(Ck-09/32); Mitotic defects in brain: cytokinesis defect (no overcondensation of diploids, very high polyploidy); Mitotic defects in brain: cytokinesis defect(very high polyploidy); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic:  
 20 Ck05/07); Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy); Mitotic defects in brain: cytokinesis defect (very high polyploidy, chromosomes entangled?); Mitotic defects in brain: cytokinesis defect (very high polyploidy; Meiotic defects in testis: cytokinesis defects (Ck-04/06) `; Female sterile (anaphase bridges, lagging chromosomes); Mitotic defects in brain: cytokinesis defect.  
 25 Meiotic defects in testis: cytokinesis defects:(mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: cytokinesis defects(Ck-06/09); Meiotic defects in testis: segregation defects, cytokinesis defect(Ck-07/35); Meiotic defects in testis: cytokinesis defects.

Alternatively, mutations in the polypeptides and polynucleotides of the invention may be associated with a failure to enter M-phase; such polypeptides and polynucleotides are conveniently categorised as "Category 2". Phenotypes associated with Category 2 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Meiotic defects in testis: no division(no meiosis); Mitotic defects in brain: no mitosis; Meiotic defects in testis: segregation defects, meiotic failure(Mf-07/75); Meiotic defects in testis: segregation defects, meiotic failure(Mf-05/31); Meiotic defects in testis: cytokinesis defects, meiotic failure(Mf-02/15).

Mutations in the polypeptides and polynucleotides of the invention may be associated with a metaphase arrest phenotype ("Category 3"). Phenotypes associated with Category 3 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: prometaphase arrest (overcondensation, polyploidy, scattered chromosomes with bipolar spindle); Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest (Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle); Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle); Mitotic defects in brain: prometaphase arrest; Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: metaphase arrest.(overcondensation, polyploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle); Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest (overcondensation, metaphase with bipolar spindle; Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29); Meiotic defects in testis: cytokinesis defects, abnormal spindles.(Ab-01/03); Mitotic defects in brain: metaphase arrest; Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle); Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles (mitotic: High mitotic index, meiotic: Ab-08/24); Mitotic defects in brain: metaphase arrest(overcondensation, few anaphases, some polyploids); Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar spindle);

Mitotic defects in brain: metaphase arrest(condensation, no polyploidy, no anaphases, metaphase with bipolar spindle).

Mutations in Category 4 polypeptides and polynucleotides of the invention may be associated with an anaphase defect phenotype; phenotypes associated with Category 4

5 polypeptides and polynucleotides include any one or more of the following, singly or in combination: Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes); Meiotic defects in testis: segregation defects; Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect; Mitotic defects in brain: anaphase defects(overcondensation, anaphase

10 bridge, metaphase with swollen chromosomes and bipolar spindle); Mitotic defects in brain: Anaphase defects. (overcondensation, aneuploidy, some lagging chromosomes and breaks); Meiotic defects in testis: segregation defects; Meiotic defects in testis: segregation defects, multi-stage defects (PI-02/17); Meiotic defects in testis: segregation defects, multi-stage defects (PI-02/18); Meiotic defects in testis: cytokinesis defects,

15 segregation defects (seg-01/01); Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects Polyploidy, no overcondensation PI-01/10; Meiotic defects in testis: segregation defects, abnormal spindles. (Ab-03/30); Mitotic defects in brain: anaphase defects (weak, higher condensation, some polyploidy, fewer anaphases, polyploids with monopolar spindles); Mitotic defects in brain: anaphase

20 defects (overcondensation, polyploidy (with overcondensation), few anaphases, metaphase with bipolar spindle); Meiotic defects in testis: cytokinesis defects; Meiotic defects in testis: segregation defects,multipolar spindles(Mul-02/22); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-04/26); Meiotic defects in testis: cytokinesis defects,abnormal spindles (Ab-16/13); Mitotic defects in brain: anaphase defects. Meiotic

25 defects in testis: segregation defects, abnormal spindles (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20 ); Meiotic defects in testis: segregation defects; Meiotic defects in testis: no division (no meiosis); Meiotic defects in testis: segregation defects, abnormal spindles (Ab-12/48); Meiotic defects in testis: segregation defects, multipolar spindles(mitotic: High polyploids,

30 no diploids, higher mitotic index Meiotic: Mul-02/59); Meiotic defects in testis: segregation defect; Meiotic defects in testis: segregation defects,abnormal spindles

(meiotic: Ab-08/42); Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02; Mitotic defects in brain: anaphase defects; Meiotic defects in testis: cytokinesis defects, abnormal spindles (Ab-01/04); Meiotic defects in testis: segregation defects (overcondensation, fewer anaphases); Mitotic defects in brain: (some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle).

A fifth category ("Category 5") of polypeptides and polynucleotides of the invention are associated with the presence of small imaginal discs (block to proliferation). Phenotypes associated with Category 5 polypeptides and polynucleotides include any one or more of the following, singly or in combination: 2nd chromosome, small imaginal discs.

The polypeptides and polynucleotides of the invention may also be categorised according to their function, or their putative function.

For example, the polypeptides described here preferably comprise, and the polynucleotides described here are ones which preferably encode polypeptides comprising, any one or more of the following: a CBP activator protein; a CCR4-associated regulator of polymerase II transcription; a CTP synthase (CTPS); a Cyclin specific ubiquitin conjugating enzyme; a DNA packaging protein; a DNA repair protein; a DNA-binding protein involved in chromosomal organisation; a DNase IV; a EIF4G2 translation initiation factor; a eukaryotic translation initiation factor 6; a Ecdysone-induced protein 78C; a Egf2 translation factor; a G protein-coupled receptor kinase 7; a GTPase exchange factor; a phosphatidylinositol transfer protein beta isoform; a His-rich protein; a Lk6 kinase; a MAP kinase; a MAP kinase interacting kinase 1; a N-arginine dibasic convertase; a Phosphatidylinositol transfer protein; a RIP protein kinase; a RNA binding motif, single stranded interacting protein; a RNA binding protein; a RYK receptor tyrosine kinase; a Ribosomal protein L1; a selenide, water dikinase 1; a selenium donor protein 1; a selenophosphate synthetase 1; a Sqv-7-like protein; a sugar modification protein; a protein involved in cytokinesis and signalling; a TEK tyrosine kinase; a Translation elongation

factor; a UDP-galactose transporter; a v-erba related protein; a WD40 protein; a brahma protein; a calcium binding protein; a cell adhesion protein; a chaperone; a chromodomain helicase DNA binding protein; a chromodomain-helicase-DNA-binding protein; a coiled coil protein with ubiquitin like domain; a component of the 19S proteasome regulatory  
5 particle; a couch potato RNA binding protein; a cytidine 5-prime triphosphate synthetase; a cytoskeletal structural protein; a death domain containing protein; a developmentally expressed in axons of the CNS; a diacylglycerol-activated/phospholipid dependent protein kinase C inhibitor; a diazepam binding inhibitor; a diphosphate kinase; a dodecasatellite DNA binding protein; a doughnut protein tyrosine kinase; an elongation factor 2; a  
10 endoplasmic reticulum ATPase; a eukaryotic translation initiation factor 4E binding protein 2; a factor involved in axon guidance; a fatty-acid-Coenzyme A ligase; a flap structure-specific endonuclease 1; a protein involved in the formation of the contractile ring and the initiation of cytokinesis; a glucose-6-phosphate transporter; a glycoprotein glucosyltransferase; a growth factor; a transmembrane receptor protein tyrosine kinase  
15 involved in cell growth and maintenance; a guanyl-nucleotide exchange factor involved in signal transduction; a heat shock protein; a helicase; a high density lipoprotein binding protein; a histone acetyl transferase transcriptional activator; a histone acetyltransferase; a histone acetyltransferase GCN5; a protein involved in development of the abdomen (embryos); a protein involved in the development of the imaginal discs (larvae or pupae);  
20 a kinesin like protein 67a; a ligand-dependent nuclear receptor; a ligand-dependent nuclear receptor; a lola-like specific RNA polymerase II transcription factor; a matrix associated protein; a membrane glycoprotein; a mitotic heterochromatin fragment clone CH(2)6; a motor protein; a motor protein involved in cytoskeleton organization; a mushroom body RNA binding protein; a myosin like proteins; a nemo-like kinase; a non-ATPase protein; a  
25 nuclear receptor NR1E1; a nucleic acid binding protein; a nucleoside diphosphate kinase (NBR-A); a oly(rC)-binding protein 2 (hnRNP-E1); a peroxisome biogenesis factor 1; a phospholipid transporter involved in lipid metabolism; a phosphatase or enhancer of Pi uptake protein; a protease; a proteasome regulatory particle; a protein involved in cytoskeleton organization and/or biogenesis; a protein kinase associated with  
30 microtubules; a protein kinase mitogen-activated 7; a protein serine/threonine kinase involved in cell cycle, possibly targeted to cytoskeleton; a protein serine/threonine kinase involved in eye morphogenesis; a protein which associates with cdc25 phosphatase; a



protein which induces apoptosis; a ribonuclease P; a ribonuclease P protein subunit p29; a ser/thr phosphatase; a signal transduction protein; a signal transport protein; a sin3-associated polypeptide; a single stranded DNA/RNA binding protein; a sodium-dependent dicarboxylate transporters; a ssDNA/RNA binding proteins; a striatin, calmodulin-binding protein (STRN); a structural protein of ribosome involved in protein biosynthesis; a subtelomeric heterochromatin repeats; a sugar acetylase; a sugar modification protein; a suppressor of ras; a tRNA processing enzyme Ribonuclease P protein subunit; a thyroid hormone responsive gene; a tie receptor protein tyrosine kinase; a transacylase; a transcription factor; a transcription factor involved in chromatin remodelling; a transcriptional regulation of c-myc expression; a transcriptional regulator; a transcriptional regulators/telomeric silencing; a translation initiation factor; a tumor metastasis inhibitor; a tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein; a ubiquitin carrier protein; a ubiquitin-conjugating enzyme; a ugtUDP-glucose-glycoprotein glucosyltransferase; a zinc finger protein; an RNA polymerase II transcription factor; an acetylcholinesterase (YT blood group) precursor; an actin binding protein; an actin dependent regulator of chromatin; an acyl-CoA-binding protein; an alanine:glyoxylate aminotransferase; an alpha esterase; an ankyrin protein; an imitation-SWI protein; and an integrin beta 4 binding protein.

#### POLYPEPTIDES

- 20 It will be understood that polypeptides of the invention are not limited to polypeptides having the amino acid sequence set out in Examples 1 to 70 or fragments thereof but also include homologous sequences obtained from any source, for example related viral/bacterial proteins, cellular homologues and synthetic peptides, as well as variants or derivatives thereof.
- 25 Thus polypeptides of the invention also include those encoding homologues from other species including animals such as mammals (e.g. mice, rats or rabbits), especially primates, more especially humans. More specifically, homologues included within the scope of the invention include human homologues.

Thus, the present invention covers variants, homologues or derivatives of the amino acid sequence set out in Examples 1 to 70, as well as variants, homologues or derivatives of the nucleotide sequence coding for the amino acid sequences of the present invention.

5           In the context of the present invention, a homologous sequence is taken to include an amino acid sequence which is at least 15, 20, 25, 30, 40, 50, 60, 70, 80 or 90% identical, preferably at least 95 or 98% identical at the amino acid level over at least 50 or 100, preferably 200, 300, 400 or 500 amino acids with any one of the polypeptide sequences shown in the Examples. In particular, homology should typically be considered  
10   with respect to those regions of the sequence known to be essential for protein function rather than non-essential neighbouring sequences. This is especially important when considering homologous sequences from distantly related organisms.

          Although homology can also be considered in terms of similarity (i.e. amino acid residues having similar chemical properties/functions), in the context of the present  
15   invention it is preferred to express homology in terms of sequence identity.

          Homology comparisons can be conducted by eye, or more usually, with the aid of readily available sequence comparison programs. These publicly and commercially available computer programs can calculate % homology between two or more sequences.

          % homology may be calculated over contiguous sequences, i.e. one sequence is  
20   aligned with the other sequence and each amino acid in one sequence directly compared with the corresponding amino acid in the other sequence, one residue at a time. This is called an "ungapped" alignment. Typically, such ungapped alignments are performed only over a relatively short number of residues (for example less than 50 contiguous amino acids).

25           Although this is a very simple and consistent method, it fails to take into consideration that, for example, in an otherwise identical pair of sequences, one insertion or deletion will cause the following amino acid residues to be put out of alignment, thus

potentially resulting in a large reduction in % homology when a global alignment is performed. Consequently, most sequence comparison methods are designed to produce optimal alignments that take into consideration possible insertions and deletions without penalising unduly the overall homology score. This is achieved by inserting “gaps” in the sequence alignment to try to maximise local homology.

However, these more complex methods assign “gap penalties” to each gap that occurs in the alignment so that, for the same number of identical amino acids, a sequence alignment with as few gaps as possible - reflecting higher relatedness between the two compared sequences - will achieve a higher score than one with many gaps. “Affine gap costs” are typically used that charge a relatively high cost for the existence of a gap and a smaller penalty for each subsequent residue in the gap. This is the most commonly used gap scoring system. High gap penalties will of course produce optimised alignments with fewer gaps. Most alignment programs allow the gap penalties to be modified. However, it is preferred to use the default values when using such software for sequence comparisons. For example when using the GCG Wisconsin Bestfit package (see below) the default gap penalty for amino acid sequences is -12 for a gap and -4 for each extension.

Calculation of maximum % homology therefore firstly requires the production of an optimal alignment, taking into consideration gap penalties. A suitable computer program for carrying out such an alignment is the GCG Wisconsin Bestfit package (University of Wisconsin, U.S.A; Devereux *et al.*, 1984, Nucleic Acids Research 12:387). Examples of other software than can perform sequence comparisons include, but are not limited to, the BLAST package (see Ausubel *et al.*, 1999 *ibid* – Chapter 18), FASTA (Atschul *et al.*, 1990, J. Mol. Biol., 403-410) and the GENWORKS suite of comparison tools. Both BLAST and FASTA are available for offline and online searching (see Ausubel *et al.*, 1999 *ibid*, pages 7-58 to 7-60). However it is preferred to use the GCG Bestfit program.

Although the final % homology can be measured in terms of identity, the alignment process itself is typically not based on an all-or-nothing pair comparison. Instead, a scaled similarity score matrix is generally used that assigns scores to each

pairwise comparison based on chemical similarity or evolutionary distance. An example of such a matrix commonly used is the BLOSUM62 matrix - the default matrix for the BLAST suite of programs. GCG Wisconsin programs generally use either the public default values or a custom symbol comparison table if supplied (see user manual for  
5 further details). It is preferred to use the public default values for the GCG package, or in the case of other software, the default matrix, such as BLOSUM62.

Once the software has produced an optimal alignment, it is possible to calculate % homology, preferably % sequence identity. The software typically does this as part of the sequence comparison and generates a numerical result.

10 The terms "variant" or "derivative" in relation to the amino acid sequences of the present invention includes any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) amino acids from or to the sequence providing the resultant amino acid sequence retains substantially the same activity as the unmodified  
15 sequence listings in the Examples.

Polypeptides having the amino acid sequence shown in the Examples, or fragments or homologues thereof may be modified for use in the present invention. Typically, modifications are made that maintain the biological activity of the sequence. Amino acid substitutions may be made, for example from 1, 2 or 3 to 10, 20 or 30 substitutions  
20 provided that the modified sequence retains the biological activity of the unmodified sequence. Alternatively, modifications may be made to deliberately inactivate one or more functional domains of the polypeptides of the invention. Amino acid substitutions may include the use of non-naturally occurring analogues, for example to increase blood plasma half-life of a therapeutically administered polypeptide.

25 Conservative substitutions may be made, for example according to the Table below. Amino acids in the same block in the second column and preferably in the same line in the third column may be substituted for each other:

ALIPHATIC	Non-polar	G A P
		I L V
	Polar - uncharged	C S T M
		N Q
	Polar - charged	D E
		K R
AROMATIC		H F W Y

Polypeptides of the invention also include fragments of the full length sequences mentioned above. Preferably said fragments comprise at least one epitope. Methods of identifying epitopes are well known in the art. Fragments will typically comprise at least 6 amino acids, more preferably at least 10, 20, 30, 50 or 100 amino acids.

5 Proteins of the invention are typically made by recombinant means, for example as described below. However they may also be made by synthetic means using techniques well known to skilled persons such as solid phase synthesis. Proteins of the invention may also be produced as fusion proteins, for example to aid in extraction and purification. Examples of fusion protein partners include glutathione-S-transferase (GST), 6xHis,  
 10 GAL4 (DNA binding and/or transcriptional activation domains) and  $\beta$ -galactosidase. It may also be convenient to include a proteolytic cleavage site between the fusion protein partner and the protein sequence of interest to allow removal of fusion protein sequences. Preferably the fusion protein will not hinder the function of the protein of interest sequence. Proteins of the invention may also be obtained by purification of cell extracts  
 15 from animal cells.

Proteins of the invention may be in a substantially isolated form. It will be understood that the protein may be mixed with carriers or diluents which will not interfere with the intended purpose of the protein and still be regarded as substantially isolated. A protein of the invention may also be in a substantially purified form, in which case it will  
 20 generally comprise the protein in a preparation in which more than 90%, e.g. 95%, 98% or 99% of the protein in the preparation is a protein of the invention.

A polypeptide of the invention may be labeled with a revealing label. The revealing label may be any suitable label which allows the polypeptide to be detected. Suitable labels include radioisotopes, e.g. <sup>125</sup>I, enzymes, antibodies, polynucleotides and linkers such as biotin. Labeled polypeptides of the invention may be used in diagnostic procedures such as

5 immunoassays to determine the amount of a polypeptide of the invention in a sample. Polypeptides or labeled polypeptides of the invention may also be used in serological or cell-mediated immune assays for the detection of immune reactivity to said polypeptides in animals and humans using standard protocols.

A polypeptide or labeled polypeptide of the invention or fragment thereof may also

10 be fixed to a solid phase, for example the surface of an immunoassay well or dipstick. Such labeled and/or immobilised polypeptides may be packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like. Such polypeptides and kits may be used in methods of detection of antibodies to the polypeptides or their allelic or species variants by immunoassay.

15 Immunoassay methods are well known in the art and will generally comprise: (a) providing a polypeptide comprising an epitope bindable by an antibody against said protein; (b) incubating a biological sample with said polypeptide under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said polypeptide is formed.

20 Polypeptides of the invention may be used in *in vitro* or *in vivo* cell culture systems to study the role of their corresponding genes and homologues thereof in cell function, including their function in disease. For example, truncated or modified polypeptides may be introduced into a cell to disrupt the normal functions which occur in the cell. The polypeptides of the invention may be introduced into the cell by *in situ* expression of the

25 polypeptide from a recombinant expression vector (see below). The expression vector optionally carries an inducible promoter to control the expression of the polypeptide.

The use of appropriate host cells, such as insect cells or mammalian cells, is expected to provide for such post-translational modifications (e.g. myristolation,

glycosylation, truncation, lapidation and tyrosine, serine or threonine phosphorylation) as may be needed to confer optimal biological activity on recombinant expression products of the invention. Such cell culture systems in which polypeptides of the invention are expressed may be used in assay systems to identify candidate substances which interfere  
5 with or enhance the functions of the polypeptides of the invention in the cell.

### POLYNUCLEOTIDES

Polynucleotides of the invention include polynucleotides that comprise any one or more of the nucleic acid sequences set out in Examples 1 to 70 and fragments thereof. Polynucleotides of the invention also include polynucleotides encoding the polypeptides  
10 of the invention. It will be understood by a skilled person that numerous different polynucleotides can encode the same polypeptide as a result of the degeneracy of the genetic code. In addition, it is to be understood that skilled persons may, using routine techniques, make nucleotide substitutions that do not affect the polypeptide sequence encoded by the polynucleotides of the invention to reflect the codon usage of any  
15 particular host organism in which the polypeptides of the invention are to be expressed.

Polynucleotides of the invention may comprise DNA or RNA. They may be single-stranded or double-stranded. They may also be polynucleotides which include within them synthetic or modified nucleotides. A number of different types of modification to oligonucleotides are known in the art. These include methylphosphonate  
20 and phosphorothioate backbones, addition of acridine or polylysine chains at the 3' and/or 5' ends of the molecule. For the purposes of the present invention, it is to be understood that the polynucleotides described herein may be modified by any method available in the art. Such modifications may be carried out in order to enhance the *in vivo* activity or life span of polynucleotides of the invention.

25 The terms "variant", "homologue" or "derivative" in relation to the nucleotide sequence of the present invention include any substitution of, variation of, modification of, replacement of, deletion of or addition of one (or more) nucleic acid from or to the

sequence. Preferably said variant, homologues or derivatives code for a polypeptide having biological activity.

As indicated above, with respect to sequence homology, preferably there is at least 50 or 75%, more preferably at least 85%, more preferably at least 90% homology to the sequences shown in the sequence listing herein. More preferably there is at least 95%, more preferably at least 98%, homology. Nucleotide homology comparisons may be conducted as described above. A preferred sequence comparison program is the GCG Wisconsin Bestfit program described above. The default scoring matrix has a match value of 10 for each identical nucleotide and -9 for each mismatch. The default gap creation penalty is -50 and the default gap extension penalty is -3 for each nucleotide.

The present invention also encompasses nucleotide sequences that are capable of hybridising selectively to the sequences presented herein, or any variant, fragment or derivative thereof, or to the complement of any of the above. Nucleotide sequences are preferably at least 15 nucleotides in length, more preferably at least 20, 30, 40 or 50 nucleotides in length.

The term "hybridization" as used herein shall include "the process by which a strand of nucleic acid joins with a complementary strand through base pairing" as well as the process of amplification as carried out in polymerase chain reaction technologies.

Polynucleotides of the invention capable of selectively hybridising to the nucleotide sequences presented herein, or to their complement, will be generally at least 70%, preferably at least 80 or 90% and more preferably at least 95% or 98% homologous to the corresponding nucleotide sequences presented herein over a region of at least 20, preferably at least 25 or 30, for instance at least 40, 60 or 100 or more contiguous nucleotides.

The term "selectively hybridizable" means that the polynucleotide used as a probe is used under conditions where a target polynucleotide of the invention is found to hybridize to the probe at a level significantly above background. The background



hybridization may occur because of other polynucleotides present, for example, in the cDNA or genomic DNA library being screening. In this event, background implies a level of signal generated by interaction between the probe and a non-specific DNA member of the library which is less than 10 fold, preferably less than 100 fold as intense as the  
5 specific interaction observed with the target DNA. The intensity of interaction may be measured, for example, by radiolabelling the probe, e.g. with  $^{32}\text{P}$ .

Hybridization conditions are based on the melting temperature ( $T_m$ ) of the nucleic acid binding complex, as taught in Berger and Kimmel (1987, Guide to Molecular Cloning Techniques, Methods in Enzymology, Vol 152, Academic Press, San Diego CA), and  
10 confer a defined "stringency" as explained below.

Maximum stringency typically occurs at about  $T_m - 5^\circ\text{C}$  ( $5^\circ\text{C}$  below the  $T_m$  of the probe); high stringency at about  $5^\circ\text{C}$  to  $10^\circ\text{C}$  below  $T_m$ ; intermediate stringency at about  $10^\circ\text{C}$  to  $20^\circ\text{C}$  below  $T_m$ ; and low stringency at about  $20^\circ\text{C}$  to  $25^\circ\text{C}$  below  $T_m$ . As will be understood by those of skill in the art, a maximum stringency hybridization can be used to  
15 identify or detect identical polynucleotide sequences while an intermediate (or low) stringency hybridization can be used to identify or detect similar or related polynucleotide sequences.

In a preferred aspect, the present invention covers nucleotide sequences that can hybridise to the nucleotide sequence of the present invention under stringent conditions  
20 (e.g.  $65^\circ\text{C}$  and  $0.1\times\text{SSC}$  { $1\times\text{SSC} = 0.15\text{ M NaCl}$ ,  $0.015\text{ M Na}_3\text{ Citrate pH } 7.0$ }).

Where the polynucleotide of the invention is double-stranded, both strands of the duplex, either individually or in combination, are encompassed by the present invention. Where the polynucleotide is single-stranded, it is to be understood that the complementary sequence of that polynucleotide is also included within the scope of the present invention.

25 Polynucleotides which are not 100% homologous to the sequences of the present invention but fall within the scope of the invention can be obtained in a number of ways. Other variants of the sequences described herein may be obtained for example by probing

DNA libraries made from a range of individuals, for example individuals from different populations. In addition, other viral/bacterial, or cellular homologues particularly cellular homologues found in mammalian cells (e.g. rat, mouse, bovine and primate cells), may be obtained and such homologues and fragments thereof in general will be capable of

5 selectively hybridising to the sequences shown in the Examples. Such sequences may be obtained by probing cDNA libraries made from or genomic DNA libraries from other animal species, and probing such libraries with probes comprising all or part of any one of the sequences shown in the Examples under conditions of medium to high stringency. The nucleotide sequences of the human homologues described in the Examples, may

10 preferably be used to identify other primate/mammalian homologues since nucleotide homology between human sequences and mammalian sequences is likely to be higher than is the case for the *Drosophila* sequences identified herein.

Similar considerations apply to obtaining species homologues and allelic variants of the polypeptide or nucleotide sequences of the invention.

15 Variants and strain/species homologues may also be obtained using degenerate PCR which will use primers designed to target sequences within the variants and homologues encoding conserved amino acid sequences within the sequences of the present invention. Conserved sequences can be predicted, for example, by aligning the amino acid sequences from several variants/homologues. Sequence alignments can be performed

20 using computer software known in the art. For example the GCG Wisconsin PileUp program is widely used.

The primers used in degenerate PCR will contain one or more degenerate positions and will be used at stringency conditions lower than those used for cloning sequences with single sequence primers against known sequences. It will be appreciated by the skilled

25 person that overall nucleotide homology between sequences from distantly related organisms is likely to be very low and thus in these situations degenerate PCR may be the method of choice rather than screening libraries with labeled fragments the sequences disclosed in the Examples.

In addition, homologous sequences may be identified by searching nucleotide and/or protein databases using search algorithms such as the BLAST suite of programs. This approach is described in the Examples.

Alternatively, such polynucleotides may be obtained by site directed mutagenesis of characterised sequences, such as the sequences disclosed in the Examples. This may be useful where for example silent codon changes are required to sequences to optimise codon preferences for a particular host cell in which the polynucleotide sequences are being expressed. Other sequence changes may be desired in order to introduce restriction enzyme recognition sites, or to alter the property or function of the polypeptides encoded by the polynucleotides. For example, further changes may be desirable to represent particular coding changes found in the sequences disclosed in the Examples which give rise to mutant genes which have lost their regulatory function. Probes based on such changes can be used as diagnostic probes to detect such mutants.

Polynucleotides of the invention may be used to produce a primer, e.g. a PCR primer, a primer for an alternative amplification reaction, a probe e.g. labeled with a revealing label by conventional means using radioactive or non-radioactive labels, or the polynucleotides may be cloned into vectors. Such primers, probes and other fragments will be at least 8, 9, 10, or 15, preferably at least 20, for example at least 25, 30 or 40 nucleotides in length, and are also encompassed by the term polynucleotides of the invention as used herein.

Polynucleotides such as a DNA polynucleotides and probes according to the invention may be produced recombinantly, synthetically, or by any means available to those of skill in the art. They may also be cloned by standard techniques.

In general, primers will be produced by synthetic means, involving a step wise manufacture of the desired nucleic acid sequence one nucleotide at a time. Techniques for accomplishing this using automated techniques are readily available in the art.

Longer polynucleotides will generally be produced using recombinant means, for example using a PCR (polymerase chain reaction) cloning techniques. This will involve making a pair of primers (e.g. of about 15 to 30 nucleotides) flanking a region of the lipid targeting sequence which it is desired to clone, bringing the primers into contact with mRNA or cDNA obtained from an animal or human cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified fragment (e.g. by purifying the reaction mixture on an agarose gel) and recovering the amplified DNA. The primers may be designed to contain suitable restriction enzyme recognition sites so that the amplified DNA can be cloned into a suitable cloning vector

Polynucleotides or primers of the invention may carry a revealing label. Suitable labels include radioisotopes such as  $^{32}\text{P}$  or  $^{35}\text{S}$ , enzyme labels, or other protein labels such as biotin. Such labels may be added to polynucleotides or primers of the invention and may be detected using by techniques known *per se*.

Polynucleotides or primers of the invention or fragments thereof labeled or unlabeled may be used by a person skilled in the art in nucleic acid-based tests for detecting or sequencing polynucleotides of the invention in the human or animal body.

Such tests for detecting generally comprise bringing a biological sample containing DNA or RNA into contact with a probe comprising a polynucleotide or primer of the invention under hybridising conditions and detecting any duplex formed between the probe and nucleic acid in the sample. Such detection may be achieved using techniques such as PCR or by immobilising the probe on a solid support, removing nucleic acid in the sample which is not hybridised to the probe, and then detecting nucleic acid which has hybridised to the probe. Alternatively, the sample nucleic acid may be immobilised on a solid support, and the amount of probe bound to such a support can be detected. Suitable assay methods of this and other formats can be found in for example WO89/03891 and WO90/13667.

Tests for sequencing nucleotides of the invention include bringing a biological sample containing target DNA or RNA into contact with a probe comprising a polynucleotide or primer of the invention under hybridising conditions and determining the sequence by, for example the Sanger dideoxy chain termination method (see  
5 Sambrook *et al.*).

Such a method generally comprises elongating, in the presence of suitable reagents, the primer by synthesis of a strand complementary to the target DNA or RNA and selectively terminating the elongation reaction at one or more of an A, C, G or T/U residue; allowing strand elongation and termination reaction to occur; separating out  
10 according to size the elongated products to determine the sequence of the nucleotides at which selective termination has occurred. Suitable reagents include a DNA polymerase enzyme, the deoxynucleotides dATP, dCTP, dGTP and dTTP, a buffer and ATP. Dideoxynucleotides are used for selective termination.

Tests for detecting or sequencing nucleotides of the invention in a biological  
15 sample may be used to determine particular sequences within cells in individuals who have, or are suspected to have, an altered gene sequence, for example within cancer cells including leukaemia cells and solid tumours such as breast, ovary, lung, colon, pancreas, testes, liver, brain, muscle and bone tumours. Cells from patients suffering from a proliferative disease may also be tested in the same way.

20 In addition, the identification of the genes described in the Examples will allow the role of these genes in hereditary diseases to be investigated. In general, this will involve establishing the status of the gene (e.g. using PCR sequence analysis), in cells derived from animals or humans with, for example, neurological disorders or neoplasms.

The probes of the invention may conveniently be packaged in the form of a test kit  
25 in a suitable container. In such kits the probe may be bound to a solid support where the assay format for which the kit is designed requires such binding. The kit may also contain suitable reagents for treating the sample to be probed, hybridising the probe to nucleic acid in the sample, control reagents, instructions, and the like.

**NUCLEIC ACID VECTORS**

Polynucleotides of the invention can be incorporated into a recombinant replicable vector. The vector may be used to replicate the nucleic acid in a compatible host cell. Thus in a further embodiment, the invention provides a method of making polynucleotides of the invention by introducing a polynucleotide of the invention into a replicable vector, introducing the vector into a compatible host cell, and growing the host cell under conditions which bring about replication of the vector. The vector may be recovered from the host cell. Suitable host cells include bacteria such as *E. coli*, yeast, mammalian cell lines and other eukaryotic cell lines, for example insect Sf9 cells.

Preferably, a polynucleotide of the invention in a vector is operably linked to a control sequence that is capable of providing for the expression of the coding sequence by the host cell, i.e. the vector is an expression vector. The term "operably linked" means that the components described are in a relationship permitting them to function in their intended manner. A regulatory sequence "operably linked" to a coding sequence is ligated in such a way that expression of the coding sequence is achieved under condition compatible with the control sequences.

The control sequences may be modified, for example by the addition of further transcriptional regulatory elements to make the level of transcription directed by the control sequences more responsive to transcriptional modulators.

Vectors of the invention may be transformed or transfected into a suitable host cell as described below to provide for expression of a protein of the invention. This process may comprise culturing a host cell transformed with an expression vector as described above under conditions to provide for expression by the vector of a coding sequence encoding the protein, and optionally recovering the expressed protein. Vectors will be chosen that are compatible with the host cell used.

The vectors may be for example, plasmid or virus vectors provided with an origin of replication, optionally a promoter for the expression of the said polynucleotide and

optionally a regulator of the promoter. The vectors may contain one or more selectable marker genes, for example an ampicillin resistance gene in the case of a bacterial plasmid or a neomycin resistance gene for a mammalian vector. Vectors may be used, for example, to transfect or transform a host cell.

- 5           Control sequences operably linked to sequences encoding the polypeptide of the invention include promoters/enhancers and other expression regulation signals. These control sequences may be selected to be compatible with the host cell for which the expression vector is designed to be used in. The term promoter is well-known in the art and encompasses nucleic acid regions ranging in size and complexity from minimal  
10   promoters to promoters including upstream elements and enhancers.

- The promoter is typically selected from promoters which are functional in mammalian cells, although prokaryotic promoters and promoters functional in other eukaryotic cells, such as insect cells, may be used. The promoter is typically derived from promoter sequences of viral or eukaryotic genes. For example, it may be a promoter  
15   derived from the genome of a cell in which expression is to occur. With respect to eukaryotic promoters, they may be promoters that function in a ubiquitous manner (such as promoters of  $\alpha$ -actin,  $\beta$ -actin, tubulin) or, alternatively, a tissue-specific manner (such as promoters of the genes for pyruvate kinase). They may also be promoters that respond to specific stimuli, for example promoters that bind steroid hormone receptors. Viral  
20   promoters may also be used, for example the Moloney murine leukaemia virus long terminal repeat (MMLV LTR) promoter, the rous sarcoma virus (RSV) LTR promoter or the human cytomegalovirus (CMV) IE promoter.

- It may also be advantageous for the promoters to be inducible so that the levels of expression of the heterologous gene can be regulated during the life-time of the cell.  
25   Inducible means that the levels of expression obtained using the promoter can be regulated.

          In addition, any of these promoters may be modified by the addition of further regulatory sequences, for example enhancer sequences. Chimeric promoters may also be

used comprising sequence elements from two or more different promoters described above.

Polynucleotides according to the invention may also be inserted into the vectors described above in an antisense orientation to provide for the production of antisense  
5 RNA. Antisense RNA or other antisense polynucleotides may also be produced by synthetic means. Such antisense polynucleotides may be used in a method of controlling the levels of RNAs transcribed from genes comprising any one of the polynucleotides of the invention.

#### HOST CELLS

10 Vectors and polynucleotides of the invention may be introduced into host cells for the purpose of replicating the vectors/polynucleotides and/or expressing the polypeptides of the invention encoded by the polynucleotides of the invention. Although the polypeptides of the invention may be produced using prokaryotic cells as host cells, it is preferred to use eukaryotic cells, for example yeast, insect or mammalian cells, in  
15 particular mammalian cells.

Vectors/polynucleotides of the invention may be introduced into suitable host cells using a variety of techniques known in the art, such as transfection, transformation and electroporation. Where vectors/polynucleotides of the invention are to be administered to animals, several techniques are known in the art, for example infection with recombinant  
20 viral vectors such as retroviruses, herpes simplex viruses and adenoviruses, direct injection of nucleic acids and biolistic transformation.

#### PROTEIN EXPRESSION AND PURIFICATION

Host cells comprising polynucleotides of the invention may be used to express polypeptides of the invention. Host cells may be cultured under suitable conditions which  
25 allow expression of the proteins of the invention. Expression of the polypeptides of the invention may be constitutive such that they are continually produced, or inducible, requiring a stimulus to initiate expression. In the case of inducible expression, protein



production can be initiated when required by, for example, addition of an inducer substance to the culture medium, for example dexamethasone or IPTG.

Polypeptides of the invention can be extracted from host cells by a variety of techniques known in the art, including enzymatic, chemical and/or osmotic lysis and  
5 physical disruption.

Polypeptides of the invention may also be produced recombinantly in an *in vitro* cell-free system, such as the TnT<sup>TM</sup> (Promega) rabbit reticulocyte system.

#### ANTIBODIES

The invention also provides monoclonal or polyclonal antibodies to polypeptides of  
10 the invention or fragments thereof. Thus, the present invention further provides a process for the production of monoclonal or polyclonal antibodies to polypeptides of the invention.

If polyclonal antibodies are desired, a selected mammal (e.g., mouse, rabbit, goat, horse, etc.) is immunised with an immunogenic polypeptide bearing an epitope(s) from a polypeptide of the invention. Serum from the immunised animal is collected and treated  
15 according to known procedures. If serum containing polyclonal antibodies to an epitope from a polypeptide of the invention contains antibodies to other antigens, the polyclonal antibodies can be purified by immunoaffinity chromatography. Techniques for producing and processing polyclonal antisera are known in the art. In order that such antibodies may be made, the invention also provides polypeptides of the invention or fragments thereof  
20 haptenised to another polypeptide for use as immunogens in animals or humans.

Monoclonal antibodies directed against epitopes in the polypeptides of the invention can also be readily produced by one skilled in the art. The general methodology for making monoclonal antibodies by hybridomas is well known. Immortal antibody-producing cell lines can be created by cell fusion, and also by other techniques such as  
25 direct transformation of B lymphocytes with oncogenic DNA, or transfection with Epstein-Barr virus. Panels of monoclonal antibodies produced against epitopes in the

polypeptides of the invention can be screened for various properties; i.e., for isotype and epitope affinity.

An alternative technique involves screening phage display libraries where, for example the phage express scFv fragments on the surface of their coat with a large variety of complementarity determining regions (CDRs). This technique is well known in the art.

Antibodies, both monoclonal and polyclonal, which are directed against epitopes from polypeptides of the invention are particularly useful in diagnosis, and those which are neutralising are useful in passive immunotherapy. Monoclonal antibodies, in particular, may be used to raise anti-idiotypic antibodies. Anti-idiotypic antibodies are immunoglobulins which carry an "internal image" of the antigen of the agent against which protection is desired.

Techniques for raising anti-idiotypic antibodies are known in the art. These anti-idiotypic antibodies may also be useful in therapy.

For the purposes of this invention, the term "antibody", unless specified to the contrary, includes fragments of whole antibodies which retain their binding activity for a target antigen. Such fragments include Fv, F(ab') and F(ab')<sub>2</sub> fragments, as well as single chain antibodies (scFv). Furthermore, the antibodies and fragments thereof may be humanised antibodies, for example as described in EP-A-239400.

Antibodies may be used in method of detecting polypeptides of the invention present in biological samples by a method which comprises: (a) providing an antibody of the invention; (b) incubating a biological sample with said antibody under conditions which allow for the formation of an antibody-antigen complex; and (c) determining whether antibody-antigen complex comprising said antibody is formed.

Suitable samples include extracts tissues such as brain, breast, ovary, lung, colon, pancreas, testes, liver, muscle and bone tissues or from neoplastic growths derived from such tissues.

Antibodies of the invention may be bound to a solid support and/or packaged into kits in a suitable container along with suitable reagents, controls, instructions and the like.

## ASSAYS

The present invention provides assays that are suitable for identifying substances  
5 which bind to polypeptides of the invention and which affect, for example, formation of the nuclear envelope, exit from the quiescent phase of the cell cycle (G0), G1 progression, chromosome decondensation, nuclear envelope breakdown, START, initiation of DNA replication, progression of DNA replication, termination of DNA replication, centrosome duplication, G2 progression, activation of mitotic or meiotic functions, chromosome  
10 condensation, centrosome separation, microtubule nucleation, spindle formation and function, interactions with microtubule motor proteins, chromatid separation and segregation, inactivation of mitotic functions, formation of contractile ring, cytokinesis functions, chromatin binding, formation of replication complexes, replication licensing, phosphorylation or other secondary modification activity, proteolytic degradation,  
15 microtubule binding, actin binding, septin binding, microtubule organising centre nucleation activity and binding to components of cell cycle signalling pathways.

In addition, assays suitable for identifying substances that interfere with binding of polypeptides of the invention, where appropriate, to components of cell division cycle machinery. This includes not only components such as microtubules but also signalling  
20 components and regulatory components as indicated above. Such assays are typically *in vitro*. Assays are also provided that test the effects of candidate substances identified in preliminary *in vitro* assays on intact cells in whole cell assays. The assays described below, or any suitable assay as known in the art, may be used to identify these substances.

According to one aspect of the invention, therefore, we provide one or more  
25 substances identified by any of the assays described below, viz, mitosis assays, meiotic assays, polypeptide binding assays, microtubule binding/polymerisation assays, microtubule purification and binding assays, microtubule organising centre (MTOC) nucleation activity assays, motor protein assay, assay for spindle assembly and function,

assays for dna replication, chromosome condensation assays, kinase assays, kinase inhibitor assays, and whole cell assays, each as described in further detail below.

#### CANDIDATE SUBSTANCES

A substance that inhibits cell cycle progression as a result of an interaction with a polypeptide of the invention may do so in several ways. For example, if the substance inhibits cell division, mitosis and/or meiosis, it may directly disrupt the binding of a polypeptide of the invention to a component of the spindle apparatus by, for example, binding to the polypeptide and masking or altering the site of interaction with the other component. A substance which inhibits DNA replication may do so by inhibiting the phosphorylation or de-phosphorylation of proteins involved in replication. For example, it is known that the kinase inhibitor 6-DMAP (6-dimethylaminopurine) prevents the initiation of replication (Blow, JJ, 1993, *J Cell Biol*122,993-1002). Candidate substances of this type may conveniently be preliminarily screened by *in vitro* binding assays as, for example, described below and then tested, for example in a whole cell assay as described below. Examples of candidate substances include antibodies which recognise a polypeptide of the invention.

A substance which can bind directly to a polypeptide of the invention may also inhibit its function in cell cycle progression by altering its subcellular localisation and hence its ability to interact with its normal substrate. The substance may alter the subcellular localisation of the polypeptide by directly binding to it, or by indirectly disrupting the interaction of the polypeptide with another component. For example, it is known that interaction between the p68 and p180 subunits of DNA polymerase alpha-primase enzyme is necessary in order for p180 to translocate into the nucleus (Mizuno et al (1998) *Mol Cell Biol*18,3552-62), and accordingly, a substance which disrupts the interaction between p68 and p180 will affect nuclear translocation and hence activity of the primase. A substance which affects mitosis may do so by preventing the polypeptide and components of the mitotic apparatus from coming into contact within the cell.

These substances may be tested using, for example the whole cells assays described below. Non-functional homologues of a polypeptide of the invention may also be tested

for inhibition of cell cycle progression since they may compete with the wild type protein for binding to components of the cell division cycle machinery whilst being incapable of the normal functions of the protein or block the function of the protein bound to the cell division cycle machinery. Such non-functional homologues may include naturally occurring mutants and modified sequences or fragments thereof.

Alternatively, instead of preventing the association of the components directly, the substance may suppress the biologically available amount of a polypeptide of the invention. This may be by inhibiting expression of the component, for example at the level of transcription, transcript stability, translation or post-translational stability. An example of such a substance would be antisense RNA or double-stranded interfering RNA sequences which suppresses the amount of mRNA biosynthesis.

Suitable candidate substances include peptides, especially of from about 5 to 30 or 10 to 25 amino acids in size, based on the sequence of the polypeptides described in the Examples, or variants of such peptides in which one or more residues have been substituted. Peptides from panels of peptides comprising random sequences or sequences which have been varied consistently to provide a maximally diverse panel of peptides may be used.

Suitable candidate substances also include antibody products (for example, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies and CDR-grafted antibodies) which are specific for a polypeptide of the invention. Furthermore, combinatorial libraries, peptide and peptide mimetics, defined chemical entities, oligonucleotides, and natural product libraries may be screened for activity as inhibitors of binding of a polypeptide of the invention to the cell division cycle machinery, for example mitotic/meiotic apparatus (such as microtubules). The candidate substances may be used in an initial screen in batches of, for example 10 substances per reaction, and the substances of those batches which show inhibition tested individually. Candidate substances which show activity in *in vitro* screens such as those described below can then be tested in whole cell systems, such as mammalian cells which will be exposed to the inhibitor and tested for inhibition of any of the stages of the cell cycle.

*Polypeptide Binding Assays*

One type of assay for identifying substances that bind to a polypeptide of the invention involves contacting a polypeptide of the invention, which is immobilised on a solid support, with a non-immobilised candidate substance determining whether and/or to what extent the polypeptide of the invention and candidate substance bind to each other. Alternatively, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

In a preferred assay method, the polypeptide of the invention is immobilised on beads such as agarose beads. Typically this is achieved by expressing the component as a GST-fusion protein in bacteria, yeast or higher eukaryotic cell lines and purifying the GST-fusion protein from crude cell extracts using glutathione-agarose beads (Smith and Johnson, 1988). As a control, binding of the candidate substance, which is not a GST-fusion protein, to the immobilised polypeptide of the invention is determined in the absence of the polypeptide of the invention. The binding of the candidate substance to the immobilised polypeptide of the invention is then determined. This type of assay is known in the art as a GST pulldown assay. Again, the candidate substance may be immobilised and the polypeptide of the invention non-immobilised.

It is also possible to perform this type of assay using different affinity purification systems for immobilising one of the components, for example Ni-NTA agarose and histidine-tagged components.

Binding of the polypeptide of the invention to the candidate substance may be determined by a variety of methods well-known in the art. For example, the non-immobilised component may be labeled (with for example, a radioactive label, an epitope tag or an enzyme-antibody conjugate). Alternatively, binding may be determined by immunological detection techniques. For example, the reaction mixture can be Western blotted and the blot probed with an antibody that detects the non-immobilised component. ELISA techniques may also be used.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final concentration used is typically from 100 to 500 µg/ml, more preferably from 200 to 300 µg/ml.

5           ***Microtubule Binding/Polymerisation Assays***

In the case of polypeptides of the invention that bind to microtubules, another type of *in vitro* assay involves determining whether a candidate substance modulates binding of a polypeptide of the invention to microtubules. Such an assay typically comprises contacting a polypeptide of the invention with microtubules in the presence or absence of  
10 the candidate substance and determining if the candidate substance has an effect on the binding of the polypeptide of the invention to the microtubules. This assay can also be used in the absence of candidate substances to confirm that a polypeptide of the invention does indeed bind to microtubules. Microtubules may be prepared and assays conducted as follows:

15           ***Microtubule Purification and Binding Assays***

Microtubules are purified from 0-3h-old *Drosophila* embryos essentially as described previously (Saunders, *et al.*, 1997). About 3 ml of embryos are homogenized with a Dounce homogenizer in 2 volumes of ice-cold lysis buffer (0.1 M Pipes/NaOH, pH6.6, 5 mM EGTA, 1 mM MgSO<sub>4</sub>, 0.9 M glycerol, 1 mM DTT, 1 mM PMSF, 1 µg/ml  
20 aprotinin, 1 µg/ml leupeptin and 1 µg/ml pepstatin). The microtubules are depolymerized by incubation on ice for 15 min, and the extract is then centrifuged at 16,000 g for 30 min at 4°C. The supernatant is recentrifuged at 135,000 g for 90 min at 4°C. Microtubules in this later supernatant are polymerized by addition of GTP to 1 mM and taxol to 20 µM and incubation at room temperature for 30 min. A 3 ml aliquot of the extract is layered on top  
25 of 3 ml 15% sucrose cushion prepared in lysis buffer. After centrifuging at 54,000g for 30 min at 20°C using a swing out rotor, the microtubule pellet is resuspended in lysis buffer.

Microtubule overlay assays are performed as previously described (Saunders *et al.*, 1997). 500 ng per lane of recombinant Asp, recombinant polypeptide, and bovine serum albumin (BSA, Sigma) are fractionated by 10% SDS-PAGE and blotted onto PVDF

membranes (Millipore). The membranes are preincubated in TBST (50mM Tris pH 7.5, 150 mM NaCl, 0.05% Tween 20) containing 5% low fat powdered milk (LFPM) for 1 h and then washed 3 times for 15 min in lysis buffer. The filters are then incubated for 30 minutes in lysis buffer containing either 1 mM GDP, 1 mM GTP, or 1 mM GTP- $\gamma$ -S.

5 MAP-free bovine brain tubulin (Molecular Probes) is polymerised at a concentration of 2  $\mu$ g/ml in lysis buffer by addition of GTP to a final concentration of 1 mM and incubated at 37°C for 30 min. The nucleotide solutions are removed and the buffer containing polymerised microtubules added to the membranes for incubation for 1h at 37°C with addition of taxol at a final concentration of 10  $\mu$ M for the final 30 min. The blots are then

10 washed 3 times with TBST and the bound tubulin detected using standard Western blot procedures using anti- $\beta$ -tubulin antibodies (Boehringer Mannheim) at 2.5  $\mu$ g/ml and the Super Signal detection system (Pierce).

It may be desirable in one embodiment of this type of assay to deplete the polypeptide of the invention from cell extracts used to produce polymerise microtubules.

15 This may, for example, be achieved by the use of suitable antibodies.

A simple extension to this type of assay would be to test the effects of purified polypeptide of the invention upon the ability of tubulin to polymerise *in vitro* (for example, as used by Andersen and Karsenti, 1997) in the presence or absence of a candidate substance (typically added at the concentrations described above). *Xenopus* cell-

20 free extracts may conveniently be used, for example as a source of tubulin.

#### ***Microtubule Organising Centre (MTOC) Nucleation Activity Assays***

Candidate substances, for example those identified using the binding assays described above, may be screening using a microtubule organising centre nucleation activity assay to determine if they are capable of disrupting MTOCs as measured by, for

25 example, aster formation. This assay in its simplest form comprises adding the candidate substance to a cellular extract which in the absence of the candidate substance has microtubule organising centre nucleation activity resulting in formation of asters.



In a preferred embodiment, the assay system comprises (i) a polypeptide of the invention and (ii) components required for microtubule organising centre nucleation activity except for functional polypeptide of the invention, which is typically removed by immunodepletion (or by the use of extracts from mutant cells). The components themselves are typically in two parts such that microtubule nucleation does not occur until the two parts are mixed. The polypeptide of the invention may be present in one of the two parts initially or added subsequently prior to mixing of the two parts.

Subsequently, the polypeptide of the invention and candidate substance are added to the component mix and microtubule nucleation from centrosomes measured, for example by immunostaining for the polypeptide of the invention and visualising aster formation by immuno-fluorescence microscopy. The polypeptide of the invention may be preincubated with the candidate substance before addition to the component mix. Alternatively, both the polypeptide of the invention and the candidate substance may be added directly to the component mix, simultaneously or sequentially in either order.

The components required for microtubule organising centre formation typically include salt-stripped centrosomes prepared as described in Moritz *et al.*, 1998. Stripping centrosome preparations with 2 M KI removes the centrosome proteins CP60, CP190, CNN and  $\gamma$ -tubulin. Of these, neither CP60 nor CP190 appear to be required for microtubule nucleation. The other minimal components are typically provided as a depleted cellular extract, or conveniently, as a cellular extract from cells with a non-functional variant of a polypeptide of the invention. Typically, labeled tubulin (usually  $\beta$ -tubulin) is also added to assist in visualising aster formation.

Alternatively, partially purified centrosomes that have not been salt-stripped may be used as part of the components. In this case, only tubulin, preferably labeled tubulin is required to complete the component mix.

Candidate substances are typically added to a final concentration of from 1 to 1000 nmol/ml, more preferably from 1 to 100 nmol/ml. In the case of antibodies, the final

concentration used is typically from 100 to 500 µg/ml, more preferably from 200 to 300 µg/ml.

The degree of inhibition of aster formation by the candidate substance may be determined by measuring the number of normal asters per unit area for control untreated cell preparation and measuring the number of normal asters per unit area for cells treated with the candidate substance and comparing the result. Typically, a candidate substance is considered to be capable of disrupting MTOC integrity if the treated cell preparations have less than 50%, preferably less than 40, 30, 20 or 10% of the number of asters found in untreated cells preparations. It may also be desirable to stain cells for  $\gamma$ -tubulin to determine the maximum number of possible MTOCs present to allow normalisation between samples.

#### ***Motor Protein Assay***

Polypeptides of the invention may interact with motor proteins such as the Eg5-like motor protein *in vitro*. The effects of candidate substances on such a process may be determined using assays wherein the motor protein is immobilised on coverslips. Rhodamine labeled microtubules are then added and their translocation can be followed by fluorescent microscopy. The effect of candidate substances may thus be determined by comparing the extent and/or rate of translocation in the presence and absence of the candidate substance. Generally, candidate substances known to bind to a polypeptide of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of motor proteins and the resulting identified substances tested for affects on a polypeptide of the invention as described above.

Typically this assay uses microtubules stabilised by taxol (e.g. Howard and Hyman 1993; Chandra and Endow, 1993 – both chapters in “Motility Assays for Motor Proteins” Ed Jon Scholey, pub Academic Press). If however, a polypeptide of the invention were to promote stable polymerisation of microtubules (see above) then these microtubules could be used directly in motility assays.

Simple protein-protein binding assays as described above, using a motor protein and a polypeptide of the invention may also be used to confirm that the polypeptide of the invention binds to the motor protein, typically prior to testing the effect of candidate substances on that interaction.

5        *Assay for Spindle Assembly and Function*

A further assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is an assay which measures spindle assembly and function. Typically, such assays are performed using *Xenopus* cell free systems, where two types of spindle assembly are possible. In the "half spindle" assembly  
10        pathway, a cytoplasmic extract of CSF arrested oocytes is mixed with sperm chromatin. The half spindles that form subsequently fuse together. A more physiological method is to induce CSF arrested extracts to enter interphase by addition of calcium, whereupon the DNA replicates and kinetochores form. Addition of fresh CSF arrested extract then induces mitosis with centrosome duplication and spindle formation (for discussion of  
15        these systems see Tournebize and Heald, 1996).

Again, generally, candidate substances known to bind to a polypeptide of the invention, or non-functional polypeptide variants of the invention, would be tested in this assay. Alternatively, a high throughput assay may be used to identify modulators of spindle formation and function and the resulting identified substances tested for affects  
20        binding of the polypeptide of the invention as described above.

*Assays for DNA Replication*

Another assay to investigate the function of polypeptide of the invention and the effect of candidate substances on those functions is as assay for replication of DNA. A number of cell free systems have been developed to assay DNA replication. These can be  
25        used to assay the ability of a substance to prevent or inhibit DNA replication, by conducting the assay in the presence of the substance. Suitable cell-free assay systems include, for example the SV-40 assay (Li and Kelly, 1984, *Proc. Natl. Acad. Sci USA* 81, 6973-6977; Waga and Stillman, 1994, *Nature* 369, 207-212.). A *Drosophila* cell free replication system, for example as described by Crevel and Cotteril (1991), *EMBO J.* 10,

4361-4369, may also be used. A preferred assay is a cell free assay derived from *Xenopus* egg low speed supernatant extracts described in Blow and Laskey (1986, *Cell* 47,577-587) and Sheehan et al. (1988, *J. Cell Biol.* 106, 1-12), which measures the incorporation of nucleotides into a substrate consisting of *Xenopus* sperm DNA or HeLa nuclei. The nucleotides may be radiolabelled and incorporation assayed by scintillation counting. Alternatively and preferably, bromo-deoxy-uridine (BrdU) is used as a nucleotide substitute and replication activity measured by density substitution. The latter assay is able to distinguish genuine replication initiation events from incorporation as a result of DNA repair. The human cell-free replication assay reported by Krude, et al (1997), *Cell* 88, 109-19 may also be used to assay the effects of substances on the polypeptides of the invention.

#### **Other In Vitro Assays**

Other assays for identifying substances that bind to a polypeptide of the invention are also provided. For example, substances which affect chromosome condensation may be assayed using the *in vitro* cell free system derived from *Xenopus* eggs, as known in the art.

Substances which affect kinase activity or proteolysis activity are of interest. It is known, for example, that temporal control of ubiquitin-proteasome mediated protein degradation is critical for normal G1 and S phase progression (reviewed in Krek 1998, *Curr Opin Genet Dev* 8, 36-42). A number of E3 ubiquitin protein ligases, designated SCFs (Skp1-cullin-F-box protein ligase complexes), confer substrate specificity on ubiquitination reactions, while protein kinases phosphorylate substrates destined for destruction and convert them into preferred targets for ubiquitin modification catalyzed by SCFs. Furthermore, ubiquitin-mediated proteolysis due to the anaphase-promoting complex/cyclosome (APC/C) is essential for separation of sister chromatids during mitosis, and exit from mitosis (Listovsky et al., 2000, *Exp Cell Res* 255, 184-191).

Substances which inhibit or affect kinase activity may be identified by means of a kinase assay as known in the art, for example, by measuring incorporation of  $^{32}\text{P}$  into a suitable peptide or other substrate in the presence of the candidate substance. Similarly,

substances which inhibit or affect proteolytic activity may be assayed by detecting increased or decreased cleavage of suitable polypeptide substrates.

Assays for these and other protein or polypeptide activities are known to those skilled in the art, and may suitably be used to identify substances which bind to a  
5 polypeptide of the invention and affect its activity.

### *Whole Cell Assays*

Candidate substances may also be tested on whole cells for their effect on cell cycle progression, including mitosis and/or meiosis. Preferably the candidate substances have been identified by the above-described *in vitro* methods. Alternatively, rapid  
10 throughput screens for substances capable of inhibiting cell division, typically mitosis, may be used as a preliminary screen and then used in the *in vitro* assay described above to confirm that the affect is on a particular polypeptide of the invention.

The candidate substance, i.e. the test compound, may be administered to the cell in several ways. For example, it may be added directly to the cell culture medium or injected  
15 into the cell. Alternatively, in the case of polypeptide candidate substances, the cell may be transfected with a nucleic acid construct which directs expression of the polypeptide in the cell. Preferably, the expression of the polypeptide is under the control of a regulatable promoter.

Typically, an assay to determine the effect of a candidate substance identified by  
20 the method of the invention on a particular stage of the cell division cycle comprises administering the candidate substance to a cell and determining whether the substance inhibits that stage of the cell division cycle. Techniques for measuring progress through the cell cycle in a cell population are well known in the art. The extent of progress through the cell cycle in treated cells is compared with the extent of progress through the cell cycle  
25 in an untreated control cell population to determine the degree of inhibition, if any. For example, an inhibitor of mitosis or meiosis may be assayed by measuring the proportion of cells in a population which are unable to undergo mitosis/meiosis and comparing this to the proportion of cells in an untreated population.

The concentration of candidate substances used will typically be such that the final concentration in the cells is similar to that described above for the *in vitro* assays.

A candidate substance is typically considered to be an inhibitor of a particular stage in the cell division cycle (for example, mitosis) if the proportion of cells undergoing that particular stage (i.e., mitosis) is reduced to below 50%, preferably below 40, 30, 20 or 10% of that observed in untreated control cell populations.

#### THERAPEUTIC USES

Many tumours are associated with defects in cell cycle progression, for example loss of normal cell cycle control. Tumour cells may therefore exhibit rapid and often aberrant mitosis. One therapeutic approach to treating cancer may therefore be to inhibit mitosis in rapidly dividing cells. Such an approach may also be used for therapy of any proliferative disease in general. Thus, since the polypeptides of the invention appear to be required for normal cell cycle progression, they represent targets for inhibition of their functions, particularly in tumour cells and other proliferative cells.

The term proliferative disorder is used herein in a broad sense to include any disorder that requires control of the cell cycle, for example, cardiovascular disorders such as restenosis and cardiomyopathy, auto-immune disorders such as glomerulonephritis and rheumatoid arthritis, dermatological disorders such as psoriasis, anti-inflammatory, anti-fungal, antiparasitic disorders such as malaria, emphysema and alopecia.

One possible approach is to express anti-sense constructs directed against polynucleotides of the invention, preferably selectively in tumour cells, to inhibit gene function and prevent the tumour cell from progressing through the cell cycle. Anti-sense constructs may also be used to inhibit gene function to prevent cell cycle progression in a proliferative cell. Another approach is to use non-functional variants of polypeptides of the invention that compete with the endogenous gene product for cellular components of cell cycle machinery, resulting in inhibition of function. Alternatively, compounds identified by the assays described above as binding to a polypeptide of the invention may

be administered to tumour or proliferative cells to prevent the function of that polypeptide. This may be performed, for example, by means of gene therapy or by direct administration of the compounds. Suitable antibodies of the invention may also be used as therapeutic agents.

5           Alternatively, double-stranded (ds) RNA is a powerful way of interfering with gene expression in a range of organisms that has recently been shown to be successful in mammals (Wianny and Zernicka-Goetz, 2000, Nat Cell Biol 2000, 2, 70-75). Double  
10           stranded RNA corresponding to the sequence of a polynucleotide according to the invention can be introduced into or expressed in oocytes and cells of a candidate organism to interfere with cell division cycle progression.

          In addition, a number of the mutations described herein exhibit aberrant meiotic phenotypes. Aberrant meiosis is an important factor in infertility since mutations that affect only meiosis and not mitosis will lead to a viable organism but one that is unable to produce viable gametes and hence reproduce. Consequently, the elucidation of genes  
15           involved in meiosis is an important step in diagnosing and preventing/treating fertility problems. Thus the polypeptides of the invention identified in mutant *Drosophila* having meiotic defects (as is clearly indicated in the Examples) may be used in methods of identifying substances that affect meiosis. In addition, these polypeptides, and corresponding polynucleotides, may be used to study meiosis and identify possible  
20           mutations that are indicative of infertility. This will be of use in diagnosing infertility problems.

#### ADMINISTRATION

          Substances identified or identifiable by the assay methods of the invention may preferably be combined with various components to produce compositions of the  
25           invention. Preferably the compositions are combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition (which may be for human or animal use). Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition of the invention may be administered by

direct injection. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration. Typically, each protein may be administered at a dose of from 0.01 to 30 mg/kg body weight, preferably from 0.1 to 10 mg/kg, more preferably from 0.1 to 1 mg/kg body weight.

- 5 Polynucleotides/vectors encoding polypeptide components (or antisense constructs) for use in inhibiting cell cycle progression, for example, inhibiting mitosis or meiosis, may be administered directly as a naked nucleic acid construct. They may further comprise flanking sequences homologous to the host cell genome. When the polynucleotides/vectors are administered as a naked nucleic acid, the amount of nucleic acid administered may typically be in the range of from 1 µg to 10 mg, preferably from 100 µg to 1 mg. It is particularly preferred to use polynucleotides/ vectors that target specifically tumour or proliferative cells, for example by virtue of suitable regulatory constructs or by the use of targeted viral vectors.

- 15 Uptake of naked nucleic acid constructs by mammalian cells is enhanced by several known transfection techniques for example those including the use of transfection agents. Example of these agents include cationic agents (for example calcium phosphate and DEAE-dextran) and lipofectants (for example lipofectam<sup>TM</sup> and transfectam<sup>TM</sup>). Typically, nucleic acid constructs are mixed with the transfection agent to produce a composition.

- 20 Preferably the polynucleotide, polypeptide, compound or vector described here may be conjugated, joined, linked, fused, or otherwise associated with a membrane translocation sequence.

- 25 Preferably, the polynucleotide, polypeptide, compound or vector, etc described here may be delivered into cells by being conjugated with, joined to, linked to, fused to, or otherwise associated with a protein capable of crossing the plasma membrane and/or the nuclear membrane (i.e., a membrane translocation sequence). Preferably, the substance of interest is fused or conjugated to a domain or sequence from such a protein responsible for the translocational activity. Translocation domains and sequences for example include



domains and sequences from the HIV-1-trans-activating protein (Tat), *Drosophila* Antennapedia homeodomain protein and the herpes simplex-1 virus VP22 protein. In a highly preferred embodiment, the substance of interest is conjugated with penetratin protein or a fragment of this. Penetratin comprises the sequence

5 RQIKIWFQNRRMKWKK and is described in Derossi, *et al.*, (1994), *J. Biol. Chem.* 269, 10444-50; use of penetratin-drug conjugates for intracellular delivery is described in WO/00/01417. Truncated and modified forms of penetratin may also be used, as described in WO/00/29427.

Preferably the polynucleotide, polypeptide, compound or vector according to the

10 invention is combined with a pharmaceutically acceptable carrier or diluent to produce a pharmaceutical composition. Suitable carriers and diluents include isotonic saline solutions, for example phosphate-buffered saline. The composition may be formulated for parenteral, intramuscular, intravenous, subcutaneous, intraocular or transdermal administration.

15 The routes of administration and dosages described are intended only as a guide since a skilled practitioner will be able to determine readily the optimum route of administration and dosage for any particular patient and condition.

The invention will now be further described by way of Examples, which are meant to serve to assist one of ordinary skill in the art in carrying out the invention and are not

20 intended in any way to limit the scope of the invention.

## EXAMPLES

### Generation and Identification of Lethal, Semi-Lethal and Sterile Third Chromosome Mutants Having Defects in Mitosis and/Or Meiosis, and Second Chromosome Mutants Having Defects in Imaginal Disc Development By P-Element

#### 5 Insertion Mutagenesis

##### *P-element mutagenesis*

Transposable elements are widely used for mutagenesis in *Drosophila melanogaster* as they couple the advantages of providing effective genetic lesions with ease of detecting disrupted genes for the purpose of molecular cloning. To achieve near  
10 saturation of the genome with mutations resulting from mobilisation of the P-lacW transposon (a P-element marked with a mini-white gene, bearing the *E.coli lacZ* gene as an enhancer trap, and an *E.coli* replicon and ampicillin resistance gene to facilitate 'plasmid rescue' of sequences at the site of the P-insertion), *Drosophila* females that are homozygous for *P-lacW* (inserted on the X chromosome) are crossed with males carrying  
15 the transposase source P( $\Delta 2-3$ ) (Deak et al., 1997). Random transpositions of the mutator element are then 'captured' in lines lacking transposase activity. Stable, or balanced, stocks bearing single lethal *P-lacW* insertions are made.

More than 41,000 lines are derived, of which approximately one-half are on the third chromosome. Originally some 3100 lethal or strong semi-lethal lines (in homozygous  
20 conditions) are identified. During preliminary characterisation unstable lines and clusters of the same mutation event are eliminated leaving 2460 lines to be characterised.

##### *Screening for Mitotic and Meiotic Defects*

About half of the mutants in the collection are embryonic lethals. We have carried out cytological screens of the 1155 lines that comprise late larval lethals, pupal lethals,  
25 pharate and adult semi-lethals for defective mitosis in the developing larval CNS. This has identified 69 mutations falling into 43 complementation groups that affect all stages of the mitotic cycle. The cytological screens involve examining orcein-stained squashed preparations of the larval CNS to detect abnormal mitotic cells. In lines where defects are

identified, the larval CNS is subjected to immunostaining to identify centromeres, spindle microtubules and DNA for further examination. This leads to clarification of the mitotic defect.

As a set of common functions are essential to both mitosis and meiosis, we then  
5 identify mutations resulting in sterility and failed progression through male meiosis. This involves examining squashed preparations larval, pupal or adult testes by phase contrast microscopy. We examine “onion stage” spermatids in the 519 pupal and pharate lethal lines and 463 adult “semi-lethal” and viable lines for variations in size and number of nuclei which provides an indication of whether there have been defects in either  
10 chromosome segregation or cytokinesis, respectively. A total of 54 lines of the 519 pupal and pharate lethal lines and 22 of the adult lines show such defects. However, another 67 lines show male sterility without having onion-stage defects. 12 lines showing onion stage defects have been scored as having mitotic defects in the independent cytological screen of squashed preparations of the larval CNS. Twelve further lines with onion stage defects  
15 show female sterility and of these, 10 show maternal effect mitotic defects in syncytial embryos. Thus greater than one half of the meiotic mutants scored appear to represent cell division functions specific to male meiosis or have targeted male germ-line specific enhancer elements, thus revealing their meiotic function but in this test not their mitotic function.

20 Further characterisation of testis preparations of each line by phase-contrast microscopy with and without staining with Hoechst to reveal DNA defined 6 broad categories of meiotic mutants:

8 mutants from the collection show defects in meiotic entry or at early stages in the first meiotic division (MF1-8).

25 18 mutants (15 complementation groups) show abnormal meiotic spindles (AB1-16). Mutants in this group almost invariably show an associated weak defect in cytokinesis, and 7 show a strong defect in spermatid differentiation. 3 of these mutants

also show mitotic defects in larval brains or in embryos derived from homozygous mutant mothers.

18 mutants (16 complementation groups) also show abnormal meiotic spindles that are strongly multipolar (MUL1-15). Three of these also show maternal effect mitotic abnormalities of multipolar spindles in syncytial embryos.

4 mutants (3 complementation groups) show strong defects at all stages of spermatogenesis from the pre-meiotic stages to spermatid elongation stages (PL1-3). In this respect they resemble the *polo*<sup>1</sup> mutation.

4 mutants show segregation defects as indicated by spermatid nuclei of heterogeneous sizes (SEG1-4). The spindles appear normal but all have what are either chromosome bridges or lagging chromosomes. One of these also shows a maternal effect.

9 mutants (7 complementation groups) show predominant cytokinesis defects. Two complementation groups also have cytokinesis defects in mitotic cells in the larval brain.

In the Examples below, the designations MF, AB, MUL, PL, SEG or CK are included in the category description where available. Further phenotype information for each mutant described in the results section is provided in the "Phenotype" field. There is considerable overlap between these categories, and it will be of much interest to distinguish between mutants in which the primary defect results in secondary consequences, and mutants that affect more than one aspect of spermatogenesis, as for example appears to be the case with *polo* mutants (Sunkel and Glover, 1988; Carmena et al, 1998).

In the Examples, lines exhibiting mitotic and meiotic phenotypes are categorised generally into four categories:

Category 1 : Failure to complete cytokinesis

Category 2 : Failure to enter M-phase

Category 3: Metaphase arrest

Category 4: Anaphase defect

Category 5: Small Imaginal Discs (Block to Proliferation; see below)

5       Category 1 phenotypes are exhibited by mutations in Examples 1 to 14; while  
Category 2 phenotypes are exhibited by mutations in Examples 15 to 19. Category 3  
phenotypes are exhibited by mutations in Examples 20 to 30, Category 4 phenotypes are  
exhibited by mutations in Examples 31 to 53. Mutations in Examples 54 to 74 exhibit a  
Category 5 phenotype.

10       *Generation and identification of second chromosome mutants having small or  
no imaginal discs.*

In the case of the second chromosome the flies used were from a second  
chromosome P-element collection established in Szeged, Hungary (Torok et al., 1993).  
The process of P-element insertion mutagenesis is essentially as described above. 15475  
15       insertions were recovered, of which 2711 were lethal or semi-lethal. After elimination of  
clusters of identical mutants, 2399 lines representing 1748 independent lethal insertions  
were recovered. Lines were chosen from the second chromosome collection on the basis  
of having small or no imaginal discs, to indicate a disruption in cell cycle progression that  
leads to underdevelopment of the discs. All the second chromosome mutants referred to in  
20       the results section are noted under the "Phenotype" field as "second chromosome, small  
imaginal discs" and comprise Category 5.

#### *Cytological Mapping of the P-Element Insertion Sites*

The site of insertion of the P-element in each mutant line was determined by *in situ*  
hybridisation of P-element DNA to salivary gland polytene chromosomes as described in  
25       Saunders et al., 1989. Wandering third stage larvae were dissected and fixed as described  
and incubated with biotin-labeled DNA made from the *P-lacW* plasmid. After signal

detection chromosomes were stained with Giemsa and examined by microscopy and signals indicating the presence of P elements were assigned to polytene chromosome bands referring to the Bridges map (Lefevre, 1976). In the majority of cases a single P element was detected, only 10% of lines having multiple (two or three) insertions. The site of insertion is given as the "Map Position" field in the results section (for example 77B)

#### ***Plasmid Rescue of P-Elements from Mutant Drosophila Lines***

Genomic DNA was isolated from adult flies by the method of Jowett et al., 1986, and plasmid rescue from the genomic DNA was performed according to Pirrotta et al., 1986. This allows the recovery of genomic DNA adjacent to the P-element which facilitates the identification of the site of P-element insertion and of genes which may be disrupted by the insertion. Essentially, genomic DNA derived from about 200 flies was digested with a restriction enzyme known to have a site within the P-element (EcoRI or SacII for cloning sequences to the left of the element, or XbaI, BglII, PstI or BamHI for sequences to the right of the element). The digested DNA was ligated overnight, and plasmids recovered by electroporation of the ligated DNA into *E.coli* XL1-blue competent cells. Appropriate primers from within the P-lacW sequence were used to determine the sequence of the genomic DNA flanking the element (on average, 400 bp of sequence were obtained). The rescue sequences are provided in the results section under the heading "Rescue sequence". Where more than one sequence was recovered, the orientation of each sequence is also given.

#### ***Sequence Analysis of P Element Insertion Lines***

Sequences flanking the insertion site of the P-element were derived by P element rescue as described above. In some cases sequence was obtained from only one side of the insertion, while in other cases sequences were obtained from both sides of the insertion.

As a first step, each P element rescue sequence was used to search a total database of *Drosophila melanogaster* sequences (database of the Berkley *Drosophila* Genome project) using the BLASTN program (which compares a nucleic acid sequence with a nucleic acid database, (Altschul and Lipman 1990)) with default parameters.

The search may identify a number of different types of match including *Drosophila* ESTs, known *Drosophila* genes and cloned genomic regions.

The ability to identify genes already known to be essential for cell cycle progression using this approach was confirmed, in this example, by the rescue sequence  
5 obtained from line 1324/8 which mapped to the 77B locus which was used to search the database. A BLASTN search identified a number of matching *Drosophila* ESTs, a match with the known cell cycle regulatory gene *polo* and a cloned genomic region designated CSC: AC018188. These matches are recorded in the results sections under the field headings "*Drosophila* ESTs", "*Drosophila* gene hit" and "Genomic hit, Accession No.",  
10 respectively. Any entries under "*Drosophila* gene hit" are further annotated with "(BLASTN with Rescue sequence)" to show that the match was obtained using the rescue sequence rather than a *Drosophila* EST or genomic clone ORF (see below). Accession numbers of ESTs, genes and genomic clones are provided where known. Genomic clones designations often include the Genbank designation as part of a longer designation.  
15 However the Genbank designation is always the code beginning with "AC" and followed by six digits.

Where an EST was identified, this was subsequently used to search using the BLASTX program (default parameters) against databases of sequences from *Drosophila* and Homo sapiens (databases of the National centre for Biotechnology Information  
20 (NCBI), National Library of Medicine, National Institute of Health, USA). In the case of line 1104/16, the search identified a known human gene, phosphatidylinositol transfer protein (accession no. P48739) implying a novel function for this protein in cytokinesis. Human Homologues identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "Human homologues" and annotated  
25 with "(BLASTX with EST)". *Drosophila* genes identified as a result of a BLASTX search using a *Drosophila* EST are shown in the results section under the heading "*Drosophila* gene hit" and annotated with "(BLASTX with EST)".

Where no *Drosophila* gene was identified using the initial BLASTN search but a matching genomic clone was found (a Bac or P1 clone often in excess of 100 kilobases), a

20 kilobase segment of this genomic sequence (10 kilobases either side flanking the site of the P-element insertion) was subjected to a number of analyses.

If the rescue sequence matched sequences that lie within a known gene present within the genomic clone then these are presented under the heading “*Drosophila* gene hit  
5 (BLASTN with Rescue sequence”. The known gene sequence was then used in a BLASTX search of a human database (NCBI – see above) to identify any human homologues. These are shown in the “Human homologue” field and annotated with “(BLASTX with *Drosophila* gene)”.

If the rescue sequence does not match any sequences that lie with a known gene  
10 within the genomic clone then the occurrence of ORFs within the 20 kilobase genomic segment was predicted using the Genscan programme (Burge and Karlin, 1997). Where the P-element was observed to be inserted into the coding region or within the 5’ untranslated region (which we defined as within 2 kilobases of the predicted start of the coding region) we assume the P element to be capable of disrupting the expression of the  
15 predicted gene. Each predicted open reading frame (or predicted coding sequence) was then used to search *Drosophila* and human databases using the TBLASTN program (compares a protein query sequence against a nucleotide sequence database dynamically translated in all reading frames) and/or the TBLASTX program (compares a nucleotide query sequence dynamically translated in all reading frames against a nucleotide sequence  
20 database dynamically translated in all reading frames) to determine whether the predicted open reading frame corresponded to a known gene. Typically, TBLASTX is only used when no matches are found using TBLASTN.

Where the TBLASTN search found a known *Drosophila* gene, then this is indicated in the results in the “*Drosophila* gene hit” field, annotated with “(TBLASTN  
25 with predicted ORF)”. The *Drosophila* gene sequence was then typically used to search a human database (NCBI – see above) to identify any human homologues using BLASTX. These are shown in the “Human homologue” field and annotated with “(BLASTX with *Drosophila* gene)”.



Where the TBLASTN and/or TBLASTX search found a known human gene, then this is indicated in the results in the "Human homologue" field, annotated with "(TBLASTN (or TBLASTX) with predicted ORF)".

5 If the TBLASTN and/or TBLASTX search found no *Drosophila* or human genes, then it was assumed that the original ORF corresponds to a novel gene. If the TBLASTN search found no *Drosophila* genes but identified a human homologue, then it was assumed that the original ORF corresponds to a novel *Drosophila* homologue of a known human gene.

10 ***Additional Sequence Analysis using the Annotated D. melanogaster Sequence (GadFly).***

Rescue sequences were also used to search the fully annotated version of the *Drosophila* genome (GadFly; Adams, et al., 2000, Science 287, 2185-2195), using GlyBLAST at the Berkeley *Drosophila* Genome Projects web site to identify the genome segment (usually approximately 200-250 kb) containing the P-element insertion site. The  
15 graphic representation of the genomic fragment available at GadFly allows the identification of all real and theoretical genes which flank the site of insertion. Candidate genes where the P-element is either inserted within the gene or close to the 5' end of the gene were identified. In GadFly, the *Drosophila* genes are given the designation CG (Complete gene) and usually details of human homologues are also given. In most cases,  
20 this data confirms the data derived from the sequence analysis procedure described above, and in some cases new data is obtained. Where available both sets of data are included in the individual Examples described below. To identify further candidate human homologues, BLASTP (amino acid query sequence against amino acid database) searches with *Drosophila* sequences are used against the human genome project database and also  
25 the Ensembl dataset. The Ensembl dataset comprises GeneWise gene predictions using a protein template where possible or Genscan followed by BLAST confirmation via protein, cDNA or EST hits. These are matched using WUBLASTP with default parameters (Altschul et al., 1990, *J Mol Biol* 215, 403-10). The results are filtered to contain only potential homologues. Only matches with the identity of more than 50% and length of  
30 more than 50 amino acids are included.

***Confirmation of Cell Cycle Involvement of Candidate Genes Using Double Stranded RNA Interference (RNAi)***

P-elements usually insert into the region 5' to a *Drosophila* gene. This means that there is sometimes more than one candidate gene affected, as the P-element can insert into the 5' regions of two diverging genes (one on each DNA strand). In order to confirm which of the candidate genes is responsible for the cell cycle phenotype observed in the fly line, we use the technique of double stranded RNA interference to specifically knock out gene expression in *Drosophila* cells in tissue culture (Clemens, et al., 2000, *Proc. Natl. Acad. Sci. USA*, 6499-6503). The overall strategy is to prepare double stranded RNA (dsRNA) specific to each gene of interest and to transfect this into Schneider's *Drosophila* line 2 to inhibit the expression of the particular gene. The dsRNA is prepared from a double stranded, gene specific PCR product with a T7 RNA polymerase binding site at each end. The PCR primers consist of 25-30 bases of gene specific sequence fused to a T7 polymerase binding site (TAATACGACTCACTATAGGGACA), and are designed to amplify a DNA fragment of around 500bp. Although this is the optimal size, the sequences in fact range from 450 bp to 650 bp. Where possible, PCR amplification is performed using genomic DNA purified from Schneider's *Drosophila* line 2 as a template. This is only feasible where the gene has an exon of 450 bp or more. In instances where the gene possesses only short exons of less than 450 bp, primers are designed in different exons and PCR amplification is performed using cDNA derived from Schneider's *Drosophila* line 2 as a template.

A sample of PCR product is analysed by horizontal gel electrophoresis and the DNA purified using a Qiagen QiaQuick PCR purification kit. 1µg of DNA is used as the template in the preparation of gene specific single stranded RNA using the Ambion T7 Megascript kit. Single stranded RNA is produced from both strands of the template and is purified and immediately annealed by heating to 90 degrees C for 15 mins followed by gradual cooling to room temperature overnight. A sample of the dsRNA is analysed by horizontal gel electrophoresis.

3µg of dsRNA is transfected into Schneider's *Drosophila* line 2 using the transfection agent, Transfect (Gibco) and the cells incubated for 72 hours prior to fixation.

The DNA content of the cells is analysed by staining with propidium iodide and standard FACS analysis for DNA content. The cells in G1 and G2/S phases of the cell cycle are visualised as two separate population peaks in normal cycling S2 cells. In each experiment, Red Fluorescent Protein dsRNA is used as a negative control. In some cases

5 the phenotype is confirmed by fixing cells on poly-lysine covered slides which are then stained for DNA using DAPI and for tubulin using an anti-tubulin antibody YL1/2 and appropriate fluorescent secondary antibody to visualise aberrant mitoses.

It should be noted that RNAi could not confirm phenotype in all cases. This is to be expected as the method relies on the ability of dsRNA to prevent new protein

10 expression. Consequently, it is necessary that S2 cells express the specific cDNA of the gene in question, and also that the protein is turned over rapidly. It would therefore probably be difficult to sufficiently reduce levels of very stable proteins using this approach.

The layout of a typical entry in the results section is shown below. Not all fields

15 present in the actual results section contain information for each individual *Drosophila* line described.

#### TYPICAL RESULTS LAYOUT

20	<b>Line ID</b>	- <i>Drosophila</i> line designation
	<b>Category</b>	- Description of phenotype
	<b>Reversion</b>	- R = revertant, NR = non revertant, ? = not determined
	<b>Map Position</b>	- according to the Bridges map (Lefevre, 1976).

25	<b>Rescue ID</b>
	<b>Rescue Sequence</b>
	[nucleotide sequence]

**Genomic hit, Accession No.**

30	<b>Associated ORF</b>
	GENSCAN_predicted_peptide [results of Genscan - amino acid sequence]
	GENSCAN_predicted_CDS [results of Genscan nucleotide sequence]

35	<b><i>Drosophila</i> Gene Hit</b>
	(BLASTN with rescue sequence)

(TBLASTN (or TBLASTX) with predicted ORF)  
(BLASTX with EST)

#### Human Homologue

- 5 (BLASTX with *Drosophila* gene)  
(TBLASTN (or TBLASTX) with predicted ORF)  
(BLASTX with EST)  
*Drosophila* EST

- 10 Annotated *Drosophila* genome genomic segment  
Annotated *Drosophila* genome Complete gene candidate  
Human homologue of Complete gene candidate

- Putative function      Derived from homologies or *Drosophila* experimental data

- 15 Confirmation by RNAi      Description of Facs analysis DNA content profile

A specific example is as follows:

- 20 **Line ID**                      1324/8  
**Category**                      Mitotic defects in brain: metaphase arrest  
   (overcondensation, some circular chromosomes, no anaphases,  
   very high mitotic index, metaphase (or less aligned) with bipolar  
25 spindle, no CP190 staining)  
**Reversion**                      R  
**Map Position**                      77B
- Rescue ID**                      B1E
- 30 **Rescue Sequence**  
GTTTTGCCCATCGATTGCACGAAAACCAAGCACAAAGCGGAGAACGCGCCGA  
AACCGTTCGATTTTTTAAATGCCAAAATGAATTGGACGTGAAGCGTCAGCTGA  
ATTGGTGTGCCCGTTTCGGTGGCTATCGCACACTTTCTGGTATTTATCGCGGTA  
TTTTGTTGAGTGTTGAACAACAAATTCTATGGCCGTTACCCTTTTGAATTTACT  
35 TACTGGCGTTTACTCTGTTTGAATTGAGCGCAATATTTTTTCTATTGCTCTGC  
GCAACACTGTGTTTTAACCGCTATTTATTTGAAAATCTACAAAACTAACCGTT  
TACATTTTTGAAATTTCCAAAAGGGTTTTCCATAAATTGAGTTTTACTAAAACC  
AGTCCAACGGTCCAACTTTATATTGTTAGAAGCCCCTTTTCTAATTTGAATTG  
GCTTGCAAACGTTTTCTGAATTTAAAAATACTGCCACCCTTGTTAATTGCAGG  
40 TTTTCCGAATCCCTGATTTGTTGTTTTAAAAAGAAAATTTATTAGAAACAGCTA  
TCTCAACC

Genomic hit, Accession No. CSC:AC018188

*Drosophila* Gene Hit      Polo (X63361)

- 45 Human Homologue      BLASTX PLK-1 (P53350)

*Drosophila* EST              several including LD11851 (AA392613) which match polo

Annotated *Drosophila* genome genomic segment      AE003514

- Annotated *Drosophila* genome Complete gene candidate** CG12306  
**Human homolog of Complete gene candidate** 1e-169 1709658 P53350  
PLK1\_HUMAN  
SERINE/THREONINE-  
5 PROTEIN KINASE PLK  
(PLK-1)
- Putative function** Serine/threonine kinase known to be required for mitosis
- 10 **Confirmation by RNAi** Reduced G1 and G2/M peaks indicating fewer cycling cells, microscopy analysis of DNA and tubulin staining identified monopolar spindles characteristic of polo mutation in *Drosophila*.

**CATEGORY 1: FAILURE TO COMPLETE CYTOKINESIS**

**Example 1 (Category 1)**

5	<b>Line ID</b> 1031/14 <b>Category</b> Mitotic defects in brain: cytokinesis defect (polyploidy) <b>Reversion</b> R <b>Map Position</b> 74B
10	<b>Rescue ID</b> 2A3B <b>Rescue Sequence 1</b> CCCCCGAACATATGTTCAAGTGTGGCCGCAGCAGAGTTGTCAAAACACGCTCCC CAATGAAATAACCTAAATGTGCCATCACTGTTACTTAACAGTTTCTGTTACTTT TCTAGCGGCATGTCAAAAAAACAATAATATAGAAAATGCTAAATATATATTG 15 GACTAATGTGTTTAAATGTAACCTTACACTAGTAACAGATCCCCATTAATAAAA GCCAAACTCTAAAATTCTGCCACAAGTACTATTTCTCACGTAACACCTTACTA ACGGATTTTACATGATATCTACGACAAGAACTGTTTGCTGATATAAAATTGC TATCACCGCTTTCCGTAAACACTTTTACACTGATGGATTACAAGTTCAATTAAT ACATCAACTTACCTTAACAATTTTAAGACAATAACACTCCCACAATTTAATT 20 CAACCTACACCGCTTGATAATCAGCTGTTCTGTACAAAAACAATAACACTGT TAACAACAGCGCACAGTGGATAATACAGTCCTAAAGGCAATATACCCATTTG GCATTTTT
25	<b>Rescue ID</b> 2A3S <b>Rescue Sequence 2</b> TTCCGGGGAGAATGGCTGCGATTTTCGCGTCGGTAAAAATAGCAAATACTCGTTA ATGTGCTGTGGGAACGCTTCCTCCCCGGCCCCAAAGTGGCCCCGAAGAAAGTGA GCAAATGTGCGCGCCGCAAGATAGTCGCCGCCGAACAAACGATAGTGACGAAA GTGATTTAATTCAACTACCAGCACTCCCGCAAATACGATGAGTATGTCGCGCGG 30 CGGCAACACAACCTCTGGACTTGCAGCCGCTCCTGGCGGAGAGCGATGTCGGAA ACAGGGAGCTGGAGGAGAAGATGGGCGGATCGGCGGATCGGTCATCGCTGCTC GATGGATCCGGTTCGAAGGAGCTGAGTCACCGGGAACGCGAGGACTCGGCGTT GTTCGTCAAGAAGATCGGGAGCGCCTTGTTCTATGGCTTGTCTCCTTCATGATT ACGGTGGTAAACAAGACGGTGCTTACCTCCTACCACTTCCCCTCGTTCCTGTTCC 35 TCAGCCTCGGGCAACTTACTGCTAGCATTGTGGTCCTGGGCATGGGCAAAGCGC CTGAAAATGGTGAACCTTTTCCCTTTTGCAGAGGAATACCTTCGCCAAGATCTTT CCGCTGCCACTGATATTTCTGGGAAACATGATGTTTGACTGGGTGGCACAAAA ACCTTGAGTCTGCCCATGTTTCGCAGCCCTACGAC
40	<b>Genomic hit, Accession No.</b> AC019515  <b>Associated ORF</b> Genscan ORF1 predicted sequences:>15:31:57 GENSCAN_predicted_peptide_4 373_aa

MSMSRGGNTTLDLQPLLAESDVGNRELEEKMGGSADRSSLDDGSGSKELSHRER  
 EDSALFVKKIGSALFYGLSSFMITVVNKTVLT SYHFPSFLFLSLGQLTASIVVLGMG  
 KRLKLVNFPPLQRNTFAKIFPLPLIFLGNMMFGLGGTKTLSLPMFAALRRFSILMT  
 MLELKILGLRPSNAVQVSVYAMIGGALLAASDDL SFNMRGYIYVMITNAL TASN  
 5 GVVYKKKLDTSEIGKYGLMYNSL F MFLPALALNYVTGNLDQALNFEQWNSV  
 FVVQFLLSCVMGFILSYSTILCTQFNSALTTIVGCLKNICVTYLG MFIGGDYVFSW  
 LNCIGINISVLASLLYTYVTFRRKRAPDKQDHL PSTRGENV

>15:31:57|GENSCAN\_predicted\_CDS\_4|1122\_bp  
 10 atgagtatgtcgcgcgggcggaacacaactctggacttgagccgctcctggcggagagcgatgtcggaacaggagctgga  
 ggagaagatggcgggatcgcggaatcggtcatcgctgctgatccggctcgaaggagctgagtcaccgggaacgcgag  
 gactcggcgttgctcgaagaagatcgggagcgcttgctctatggctgtcctcctcatgattacgggtgtaacaagacgggtgc  
 ttacctctaccacttccctcgttctgttcctcagcctcgggcaacttactgtagcattgtgtcctgggcatgggcaagcgct  
 gaaattggtgaacttccccctctgcagaggaataccttcgcaagatcttccgctgccactgatattctgggaaacatgatgttg  
 15 gactgggtggcacaaaaaccttgagtctgccatgttcgcagccctacgacgcttctctatcctgatgacctgtgctggagctca  
 agatcctgggactgcgaccttgaatgcggttcaggtcagcgtatacgaatgatcggtggagcgctgctggcgccctctgatga  
 tctgtcctcaacatgaggggctacatctatgtgatgactaactgccttgaccgctcgaatggcgtatgtgaagaaaaaactc  
 gacacctcggagatcggaagtacggcctaagtactacaactcgtgttatgttctgcctgccctggccctcaactatgttacag  
 ggaatctagatcaggcgctgaacttgaacaatggaatgactcagtggttggtgcagttcctgctcagttgcgttatgggttcatc  
 20 ctatcgtacagcaccatcctgtgcagcaattcaactcggcgctgaccaccaccattgtgggatgcctgaaaaacatctgcgtaac  
 atatctgggcatgttcattggaggcgactacgtctctcgtgctcaactgtattgggatcaacatcagcgtgctggctagctgctct  
 acacgtacgtcacttttcggcggaagcggtcctccgataagcaggaccactgccagcaccgcggcgagaatgtctag

25 **Human Homologue** (TBLASTN with ORF1): KIAA0260 gene (D87449) and putative  
 Sqv-7-like protein (AJ005866)  
**Drosophila EST** CK00510 (AA140776)

**Annotated Drosophila genome genomic segment** AE003524  
**Annotated Drosophila genome Complete gene candidate** CG3874 – novel glucose-6-  
 30 phosphate transporter

**Human homologue of Complete gene candidate** EMBL:D87449 protein  
 KIAA0260\_id:BAA13390  
 gi:166578 Similar to a  
 35 C.elegans protein encoded in  
 cosmid C52E12 (U50135) and  
 Ensembl predicted gene  
 ENSG00000024527  
 Clone:AL133320  
 40 Contig:AL133320.00001  
 8.10E-95

**Putative function** Sugar modification protein similar to proteins involved in  
 Drosophila cytokinesis and signalling

45 **Confirmation by RNAi** Marked increased G1 and S peak indicating mainly arrest in  
 G1

**Example 2 (Category 1)**

5	<b>Line ID</b> <b>Category</b>	1066/5 Male semi-sterile, Meiotic defects in testis: cytokinesis defects, segregation defects. (Seg-01/62)
	<b>Reversion</b> <b>Map Position</b>	? 89B
10	<b>Rescue ID</b>	F9E
15	<b>Rescue Sequence</b>	GTATACCATTAGAGAATATGATGAAGAAGGACTGTAAGAAGATCCTTCAGTG AATTTGACTGCTGACGTCGATCGGAACCTTGCTGCGCTGACGTACAAAATCGCG AAGTGAATAAATAATATGGATGAGACCTGTTTCGCCGACATATACAATAGTG CTAAGACCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATATTT CTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTTCT TCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCAACAG CATTAAATTTGTCATGATTCTCTTAAGCGTGCACCTTATCTGAAAGTCTGAACAG CTGGCTGCGAAATGGATCCCCGGGATTGGAGATGGCAAGTAAATCTGTCCCTCG CTACAAACAAGTGGGCACCACTGGGCATTCGGGGAATAGGGATATGGGTTGG GAATGGGGATATATTGTGGCATTGGCGAAAGGTCGCTATGC

**Genomic hit, Accession No.** CSC:AC019750

25	<b>Associated ORF</b>	>16:04:57 GENSCAN_predicted_peptide_4 418_aa MKPIPNESKGTAAVGDATVVHVDVCTLFAVELDPYLRSSMGMRTTRAQSGALLL QLLAVADGGFAAHICACKCRLRLPHVTCCNRPFKATAKAKGQAVSSTKPNQL CFHGCCGWIITTKGETFTENSPTSIMSGFAWERHSLGECVVVAGTEQILLIGRTLIGR MSHTQTDSTSPFVVDCHSQLCGSKCKCICVSVGFCVRPSCQRFDMKIVWANLAM QKRFLLGAAIADMCCRNSVIWCKLQLDPVKPIDERADGSLALVTKVCDNNNIV HYVVVAGVTGSQSRSLQPLRSGQNESTEQWPRTKGGEFGFNNSRNKHSAPT QEQQELWQKQLLQDQRDDCHASGSFQSASFAETRSFTFDDTTAHSEFCFRTRAEK RRILVLLETSIKLKPDKYATSGHTRRCAIGLLHSII
35		>16:04:57 GENSCAN_predicted_CDS_4 1257_bp atgaaccattccaacgaatcaagggaacccttgcggcagttggagatgctactgtgttcacgtgtgtactttgttgcg tagagcttgatccctatctcaggagcagcatgggaatgaggacgcgtagagctcaaagcggcgtctgttattacagctccttgcg gttgccgatggaggtttgtgctcatattgtgctgcaagtgtcggctcgtttgccacatgtcacatgtgtgctgcaaccggaatcct ttcaaggcaactgcaaaagcaaaaggtcaggcggcagctccactaaaccaaacacgtttgctttcacggctgctgtgctggat aattactaccaaaaggtgaaacgttcacgaaaactcgccagcatcatgagcggttttgcgtgggagcggcatagccttggtgagt gcgtggtgtgctggaacggaacaaatcctgctgattggcaggacattgattggcgcagatgaccataactcaaacgttcgacc agcccccttgtgtgactgtcactcgcaactgtcggctccaagtgcaaatgtatctgtgtatctgtaggtttctgtgtgcgccgtct tgtcagcgccttgacatgaaaatagtttggccaacttggtatgcaaaagcgatttctattaggagcgcgaatcgccacatgtgct gccgaatcggtgattgtgtgcaaaactgcagctagatccagtcgaagcaattgacgaaagagcgcgacggcagcggtcttgact ggttaccaaagtatgcgataacaataacatcgctccactatgtgtcgttgcgtgggggttacgggcagtcagtcacggtcacggctgc
45		



aaccctccgctccggccaaaacgagtcacagaacaatggccaaggacgaagggggggaggggggattcaataacaaca  
 gcaggaacaacaaacattctgtcccacgcaagagcagcaggaactgtggcaaaaacagctgctgcaggatcaacgagacgat  
 tgtcatgccagtggagcttcagctgtcgtcattcgggagacgcgtagtttcacgttcgacgacacaaccgctcacagcgaattt  
 5 tgttttcggactagagctgagaaacggcgaattttgtgctcttgaaacatcgattaactaaaacccgataagtatgcgacaagc  
 ggtcacactcggcgatgtgcgataggattgctgcattcgattatag

- Drosophila* Gene Hit** rescue sequence: mitotic heterochromatin fragment clone CH(2)6  
 (L36595) and subtelomeric heterochromatin repeats (L03284).  
 TBLASTN with ORF1: nebula (nla) (AF147700)  
 10 **Human Homologue** BLASTX with nebula: Down Syndrome candidate region 1-like  
 protein 2 (AF176117)  
***Drosophila* EST** rescue sequence: CK01138 (AA141069)

- 15 **Annotated *Drosophila* genome genomic segment** AE003712  
**Annotated *Drosophila* genome Complete gene candidate** CG6072 - nebula  
 CG6046 - sap18

- 20 **Human homologue of Complete gene candidate** CG6072- 8e-36 'ZAKI4 a thyroid  
 hormone responsive gene in human  
 skin fibroblasts' also known as  
 DOWN SYNDROME CANDIDATE  
 REGION 1-LIKE 1; DSCR1L1  
 EMBL:D83407  
 25 protein\_id:BAA11911 gi:143504

- 30 CG6046- 3e-45 2108210 (U96915)  
 sin3 associated polypeptide p18  
 [Homo sapiens] and gi5032067  
 C7E479FFE9CA5774  
 [ref]NP\_005861.1| sin3-associated  
 polypeptide, 18kD [Homo sapiens]  
 (1.90E-43)

- 35 **Putative function** Nebula unknown function, Sap18 transcription factor

- Confirmation by RNAi** Both show reduction in G1 and G2/S peaks indicating fewer  
 cycling cells

**Line ID** 234/50  
**Category** Meiotic defects in testis: cytokinesis defects, abnormal spindles.  
(Ab-02/12)  
**Reversion** R  
5 **Map Position** 89B

**Rescue ID** 2C5E  
**Rescue Sequence**  
10 GTTTGACTGCTGACGTCGATCGGAACCTTGCTGCGCTGACGTACAAAATCGCGA  
AGTGAATAAATAATATGGATGAGACTCCTGTTTCGCCGACATATACAATAGTG  
CTCAAGACCCTAATGGAATTATACGTTAATAACCAGCCACATTTCTTAGATAT  
TTCTAATATGAGCCATCTGCTGCAGGTTCTTTCCAATATCTAATTCTAGATCTT  
CTTCGAATACGACCTTTTTGGCCATGAAACGATGATTTGCCACTTCATTCACAA  
GCATTAATTTGTCATGATTCTCTTAAGCGTGCACTTTATCTGAAAGTCTGAACA  
15 GCTGGCTGCGAAATGGATTCCCCGGATTGGAGATGGCAAGTAAATCTGTCCTC  
GCTACAAACAAGTGGGCACCACTGGGCATTCTGGGGAATAGGGATATGGGTTG  
GAAA

**Drosophila EST** rescue sequence: CK01138 (AA141069)  
20 All other entries as for 1066/5.

**Example 3 (Category 1)**

**Line ID** 1104/16  
**Category** Mitotic defects in brain: cytokinesis defect  
(no overcondensation of diploids, high polyploidy)  
**Reversion** R  
**Map Position** 92A

**Rescue ID** B5P

**Rescue Sequence 1**  
CTCCGGACACGCAGTAGCTAAATAACAACTCATTACTAGTATATTACTGCCG  
CCGATTTGCAAGCGCGTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGT  
TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT  
GATATTCGCCCCGCTGTGTGTGCGTGTGTATTTGCAAGAGAGTGTGTGTGTGT  
GTGTGCATATGACTCGTGCGTTTAGCCGACAATTGGAGAAAAAGCATTACCAA  
TCCCAATTGGCTAACTAACTAAAGTTGGCTTGGCCAAACATAAACAAAAAGT  
GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG  
ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT  
GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

**Rescue ID** B5E

**Rescue Sequence 2**  
GTCCGGAGCGGAGCTAAAGTTCGATGTTCGTGCAAAACACTTCGATTCCGATA  
GGCGGATGCTATCGATTTCCGGCGATGCCCGTTGGTCACACTTGGTGGTGGGCG  
CTGCCCCGTCGCCGACTATCGATAGCACAAGCGGGTTATTTAGGTGTGCGCAGC  
TTGTAAGGGTGACTCATGCTGTTAAAATTATTATAAAAAGTTAATGAATATAA  
TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA  
TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG  
TTTTTGAAATGTGAAATGTGGGTACCCCCAATTCTTATTCGAAATTAAATAA  
CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTTGT  
CTAGAATTCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC  
TATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA

**Genomic hit, Accession No.** AC006589

**Associated ORF**  
Genscan: ORF1 predicted sequences  
>/tmp/aaaaainga|GENSCAN\_predicted\_peptide\_2|850\_aa  
MATRGANVIWFRHGLRLHDNPALLAALADKDQGIALIPVFIFDGESAGTKNVGY  
NRMRFLLDSLQDIDDQLQAATDGRGRLLVFEGETPAYIFRRLHEQVRLHRICIEQDC  
EPIWNERDESIRSLCRELNIDFVEKVSHTLWDPQLVIETNGGIPPLTYQMFLIRCTH  
HNGDVNGDEDTGEGEGTGGRIDWAKEGACWRAGNSDEQECQACQSVSSVIMM  
VLQYSNPAHHCQLECLMTLKHNVVKDILCVVAYGTAVSRTSAKLLFYWP  
AFNANLFDKRVLLSKLTNDLVPFTCQREHCPNSGNAEAAKVCYDHSISIAYAPDC  
PPPLYLCIECANEIHREHGSLEFGDILHPMQQVSMVCENKNCRSNEKSAFSICFSTE  
CASFNNGNHPIRYCSQCHSNRHSRRGGDHVVHRSLOPAWQMDPEMQMHMVESV  
VSLLREAKPLNFEPGKESSSESCKNGSGITADNISLEERQRLGRYGIWLLVGRCTP

TADTPVEVLGRILSMLFHWFHVTA YSYDGFISCLVPHPEYARVGGHWETLASRT  
 SHLKEGLQRLICLVPEVITSEIWDYVMPHWMEAITNDVAEKELNELKIVLSKILD  
 PEMSP LGF DAKTMYNFVAIRFEKTTAKVQQQALHWLQIL TKLEILPLVQLFAMF  
 GDGVRIMKYGIQHELMREKDAQS QSLAKAPKTPCKESKETKADMANPPRPPVVE  
 5 D DSGNTSAISDDEAPN RHTEFSTDAEHNLTCCILMLDILLKQMELODVEQHMGI  
 HTSVCENV SRLIKCMVTAARVGLSSHVCALKVP IEDIIEEEKSSRKSPPESDKEKTR  
 DRDVSLSMAPLPIPLGLGGFADP

>/tmp/aaaaainga|GENSCAN\_predicted\_CDS\_2/2553\_bp  
 10 atggccacgcgagggcggaatgtgattggttcgccatggattgcgcctccatgataat  
 cccgctctattggccgcccgcgataaggatcagggtatagccctaattcccgtttcatattcgatggagagagtgcaggatcc  
 aagaatgtgggttacatcgatgcgtttcctcctggactcgttgcaggacatcgatgcagctacaggcggaactgatggacg  
 tggacgctcctggtctcgaggcggaaccggcttatctccgctcatgatgcaagtgcgtctgcacaggattgcatag  
 agcaggactcgcagccaatttggaatgagcgcgatgaaagcatccgttctctatgtcgggagctgaatacgcacttgcgagaag  
 15 gtatcacacacgcttgggatccgaattggtgattgagaccaatgtgtgcattccaccgctgacctaccaaatgttctgatacgt  
 gcacgcaccacaatggagatgtgaatgggatgaggatacgggagaaggagaagggaaccggcggaaggatgcactgggcta  
 aggaagggcgctgttgaggggcggaactccgacgaacaggaatgtcaggcctgccaatcagtgctcctggatcatgatg  
 gtgtccagtgactccaacaatccagcgcattgccagctcctggagtgcctgatgactcttaagcacaatgtcgtcaaggacatc  
 ctctgctgttggtacacggaaccgctgttcccgacctcggctgccaagctgctcttactactgcccagccttaacgccaatc  
 20 tgttcgatgcgaaagtctactctccaaactaaccaatgacctagtgcccttcacctgccaacgggagcactgtccgaactccggg  
 aatgcggaggcagcaaagggtgtgtacgaccacagcattagcatcgatcgcccgattgtccaccgcccctttacctgtgca  
 tcgagtgcgccaacgagattcatcgaggacagcgaagcctggagtgcggacattctgcatccatgcagcaggatcatgatg  
 tgtcgaaaacaagaactgtcgtccaacgagaagtcgccttctccatctgcttccacggagtgtgccagcttcaatggcaac  
 catccgatccgctactgcagccagtccacagtaataggcacaattcccgcgagggtggcgatcacgtgttccatgcagctctg  
 25 agccccgctggcagatggatccagatgcagatgcacatgtgtgagtcgggtgtaagccttctgcgagaggcgaagccacta  
 aactttgagcccggaaggagctctcgtcgtccgagtgcaaaaaaagacggctccggcatcacagctgacaatatttcttgagg  
 aacgccagagactgggacgctatgtatctggctactgttggtcgtgtacacccactgcagatactcccgtagaagtctggg  
 caggattctgagcatgctctccactggttcatgtaaccgcttactcatacagatggtttatatcctgcctggtgccacatccccgga  
 gtatgcccggttgaggagccactgggagaccttggcgtcgcgaacaagccactgaaagagggtcttcagcggttatatgcctg  
 30 gtgccatatgaggttatcacttccgaaattgggactatgtgatccgcactggatggaggccatcaccaacgacgtggccgaga  
 aggaactgaacgagctgaagattgtctcagcaagatccctgatccggaaatgtcgctctgggctttgatccaaaacatgtac  
 aactttgtggccattcgattgagaagacaacggcaagggtgcagcagcaggcactccactggctgcagatctcaccagctgg  
 agattctcattccactggctcagttgttcgcatgttcggcgatggtgttcgcataatgaatacggcatccagcacgagctgatgcg  
 cgagaaggatgccaatctcagtccttgccaaggctcccaagacccggtgtaagagagcgaaggagaccaaagcggaatg  
 35 gccaatccgccaggcctcctgtgtcaggatgactctggaatacgtctgccatttcggatgacgaggcgccacgaatcgtca  
 cacggaattctccaggtgctgagcacaatctcactgttgcacctcatgttgacatacttgaagcaaatggaactacagga  
 cgtggagcagcacatgggcatccatagagtgtcgcgagaacgtctccaggctgatcaagtgcattggtcactgcagctcaggt  
 ggggtcagtagtcatgtctgcgccttaagggttccatcgaggacatcattgaggaagaaaagctcgcgcaaatctccaccg  
 aatccgacaaggaaaagacccgtgatcgagatgttccctctcgatggctccactaccattccgctgggacctttaggaggattg  
 40 cagacccttaa

**Human Homologue** BLASTX with EST: Phosphatidylinositol transfer protein  
 (P48739)

45 **Drosophila EST** SD01527 (AI530804), GH18602 (AI387906)

**Annotated Drosophila genome genomic segment** AE003725

**Annotated *Drosophila* genome Complete gene candidate CG5269 – vib PIP transfer protein**

- 5      **Human homologue of Complete gene candidate**    1e-90 1346772 P48739  
PPI2\_HUMAN  
PHOSPHATIDYLINOSITOL  
TRANSFER PROTEIN BETA  
ISOFORM
- 10    **Putative function**      phosopolipid transporter involved in lipid metabolism
- Confirmation by RNAi**      Slight reduction of G1 and increase in G2/M peaks  
   indicating arrest in G2/M

**Line ID** 418/32  
**Category** Meiotic defects in testis: cytokinesis defects. Dark bands in eyes, dominant.  
**Reversion** ?  
 5 **Map Position** 69C

**Rescue ID** G2E

**Rescue Sequence**

10 AGCTAAATAACAAACTCATTACTAGTATATTACTGCCGCCGATTTGCAAGCGC  
 GTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGTTGTACGTCATCACTT  
 AAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATTGATATTCCGCCCGCT  
 GTGTGTGCGTGTGTATTTGCAAAAGAGTGTGTGTGTGTATGTGCATATGACTC  
 GTGCGTTTAGCCGACAATTGGAGAAAAAGCATTAGAATCCCAATTGGCTAACT  
 15 AAACTAAAGTTGGCTTGGCCAAACATAAAACAAAAAGTGCGGGCGCAGCGATT  
 TGGCAGCGAAACAAAAACACCAAAGTGTTATTGGCAGATATATATGTTAATTA  
 AATATNAAAAAGTGCGTGCGAA

**Genomic hit, Accession No.** AC006589

20 **Drosophila EST** SD01527 (AI530804), GH18602 (AI387906)

Rest of results same as line 1104/16

**Example 4 (Category 1)**

**Line ID** 1285/1  
**Category** Meiotic defects in testis: cytokinesis defects  
**Reversion** ?  
**Map Position** 85D1-5

**Rescue ID** D8E

**Rescue Sequence**

10 GTTCGCAAAAAATATATCTCACCGTGAGTGCAGAAAGAGAAAAAGAGAAGCGG  
 AGAGGTGGAGAGCAAGTGGACATGAATCGTCGAGAGTCAGAGAGAGAGAGG  
 TGGAGAGGGTGAGCAGCTGTTGTCTGACAATAACATAATCAGCAACAATTTAT  
 GCTGTTTAAAAAGAGCAAGAGAAACGCTAATGAAGGGGAACACGGGCAGGGT  
 CAGGGGTTGGTGGATCCCCTACATATCTCTCTCTTTCACCGCCCCCGCTCTGGC  
 15 ACCCTCTCTGTCTGCTCTCCCATTAGCCGCACACGTGCAAGCTTAGCATTTCTATC  
 TGTCTGTCTCTGTTTGTGTTTGTGTTTGCTAAGCCGAATTCT

**Genomic hit, Accession No.** CSC:AC014256

**Associated ORF**

Genscan ORF1 predicted sequences

>/tmp/aaaaakfaa|GENSCAN\_predicted\_peptide\_1|702\_aa

MIQRCVLLWIVCFCDLFLGLLFLKRKRNAHTPPPPQFTTYRHLLCYCFRNGEIM  
 ANICLSRLSVLEEIVLLLRVPCAFYFVDYYYVPCLLSVLSESFLYHDQLKVFNRK  
 25 QQHQQQQQQQQQQLYQQHQQQQQQHYGPPPPYFQQLHQHQHQQQQQQQQQQ  
 HQQHMKFLGGNDDRNGRGVGVGTDAIVGSRGGVSQDAADAAGAAAAAAGV  
 YVFQQRPSGGVGVGVGGVGGVGPVGAVGSTLHEAAAAEYAAHFAQKQQQT  
 RWACGDDGHGIDNPDKWKYNPPMPNANAAPGGPPGNGSNGGPGAIGTIGMGSG  
 LGGGGGGGAGGGNNGSGTNGGLHHQSMAAAAANMAAMQQAALAKHNHMI  
 30 SAAAAVAAQQHQHHPHQHPQQQQQQQQAQNQGHPHLMGGGNGLGNGNG  
 LGIHPGQQQQQQQQQQQQQHPGQYNANLLNHAAALGHMSSYAQSGGSMYDH  
 HGGAMHPGMNGGMPKQQLGPPGAGGPQDYVYMGQTTPVPMGAAMMPPQNG  
 YMNSSAVAAANRNAAITSTAKKLWEKSDGKGVSSSTPGGPLHPLQIPGIGDPSS  
 VWKDHTWSTQGENILVPPPSRAYAHGGASDTSNSGNAGILSPRDSTCAKVEYVF  
 35 SGSPTNKDSSLSGLEPHLRNLKFDDNDKSRDDKEKANSPFDTNGLKKDDQVTNSN  
 GVVNGIDDDKGFK

>/tmp/aaaaakfaa|GENSCAN\_predicted\_CDS\_1|2109\_bp

atgattcagcgctcggtgttcttctatgtagtctgcttctgcgactgttcttggggtcctgttctctaaacgtaaacgcaacgca  
 40 cactactccccccccccccgcaattcaccactatcgcatctacttcttattgttttctaatgggaaatcatggctaattttgc  
 cttagctgtctttagttagaagaattgttttctttacgctgcttctgtgcttattttgtgattattattatgtccctgtctgtgt  
 ctgtgttctcggaattcttcttaccatgaccagctcaaaagttttaatcgcaaaaacagcaacaccaacagcagcagcagcagca  
 gcagcagcaactctatcagcaacatcaacagcagcagcagcaacattacggtccaccaccgacctactttcaacagctacacca  
 gcaacaccaacagcagcagcaacaacagcagcagcagcaacaccagcaacacatgaagttttgggtggtaacgatgatcgca  
 45 atggcgcgaggagcgctggcggtggcacggatgccattgtaggatctcgaggtggcgctctcaggtatgccgccgatgcagctg  
 gtggcgccgcagccgccgctggctatgtctccagcagcgtccatcgctgtgggtggcgctcgccgctggcgaggagtg

5 ggtggcgggtgtgccaggggtcggagccgtaggctcgcacttcacgagggccgcccggcggagtagccgcccactttgcc  
 agaagcaacagcagacccgatgggcgtgcggcgacgacggccatgggatcgataacccggacaaatggaagtacaatccgc  
 cgatgaatccggccaatgcgcctcctggcggtccaccgggaaatggcagtaatggtggcccgccgattggaaccattggc  
 atgggcagcggattgggtgtgtggcgggcgaggctggcggggaaataatggcggtctgtgtacgaatggcggtctgc  
 atcatcaatcgatggcgcgtgcagctgcgaatatggcagccatgcaacaggcgggcggttgccaagcacaatcacatgat  
 cacaggcagcagccgagttgcagctcagcaacaacatcagatccacaccagcagcatcccagcagcagcagcaacagca  
 gcaggcgagcaaacaggggcatccacatcaccttatggcggtggaatggactgggcaacggcaatggattgggcatacaa  
 catccggccagcaacagcagcagcagcagcaacaacagcagcagcaacatccggccagtacaacgcaatctgcttaacc  
 atgctggctgccttgggtcacatgtcatcttatgcccaatcggtggcagcatgtacgacctatggtggagccatgcacccggg  
 10 aatgaacggcggtcatgcccagcaacagccattgggtccaccggagccggaggacccaggactatgtctacatgggtggc  
 cagaccactgtgccatgggagccgaatgatgccgccacagaatcaatatgaacagctctgtgtgagctgccaatcgga  
 atgcagcgattaccacatccactgccaagaaattgtgggagaaatccgatggcaaggcggtatcctcgagcactcccggtggac  
 cgttgcatccctgcagatcccggtcatcggtgatccctcctccgtgtggaaggatcacacctgtgtccacacagggcgagaata  
 attggtgccgccccctgcgagcctacgccatggagcgccctcgatacttcaaacagcggaatgcgggcatactgagtc  
 15 ccgcatcgcacttgcgccaagtgtgtgaatatgtttcagtggtcgcgccaccaacaagatagctcgcttccggttggaaac  
 gcatttgcgggaatctaaagttgacgacaacgataagtcacgcgacgataaggagaaagcaactctccgttgacacaaacggtt  
 tgaagaaagacgatcaggtcacaaactcaatggtgtgtcaacggcattgacgatgacaagggttcaagtga

20 **Drosophila Gene Hit** TBLASTN of ORF1: pumilio protein (L07943)  
**Human Homologue** TBLASTX with pumilio: Soares fetal heart NbHH19W Homo  
 sapiens cDNA clone (W77820)

25 **Annotated Drosophila genome genomic segment** AE003681  
**Annotated Drosophila genome Complete gene candidate** CG9755 – pumilio RNA

30 **Human homologue of Complete gene candidate** 1e-154 1944416  
 dbj|BAA19665| (D87078)  
 similar to D.melanogaster  
 pumilio protein (S22026)

35 **Putative function** Putative RNA binding protein which is localised to the cytoplasm.  
 Wild-type allele of pum involved in development of the abdomen  
 (embryos) and of the imaginal discs (larvae or pupae), perhaps  
 having a function in signal transport.

**Confirmation by RNAi** Only wild type profiles observed



**Example 5 (Category 1)**

	<b>Line ID</b>	1389/1
	<b>Category</b>	Meiotic defects in testis: segregation defect, cytokinesis defect (Ck-09/32)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	93B4-8
	<b>Rescue ID</b>	2C9P
10	<b>Rescue Sequence 1</b>	
	GTTCCGGGGTGTGTGCGTGCTTGCGAGTGTGCCTGTGTGTGTGTAGGAAAGGAG CAAGAAGCAGCAGCAGCGGCAGCAGTAGAAATAGCAAAAGGAGGCAGCAAC AACAATAAGCTAGAGAAACCGCCAGCAGCAGCCCCCTAATAAAGAGCAGAGA AAAAAATGAGTTCAAGTTGTGAAAGGTGTGTGCCGTTACACTACAACTACAA 15 CACCACCATCAGCGGCAGCAAAGAAATACAACAACAAATACGGCAATCTCCA GACAACGCGAATGTCGAAATTGTGTATACAATTTATTAAGAAAGCAAGAGCA GCAACAACAATGACCAGCTGCAGTTCATCAGCGGTGTCCTCCTGAATGCCGCT GTCGTCGTTGGTGTCTGCCACCGGCGGTTTCTCAATAATAAGGGCAGGAGGAG CTGCTTAGGTGCACACAATGTAGTTTGGCTTGGTGAATGCTTCTCTTTTGTG 20 CTGCTGGCGCATACGTTTCTCTCTCCCTCATGATCTCAGTTGTCTGCATCGA TGAGCCGCCACCAACGGTGGCTTCTTCTGCTCCTCTTTGGCAACGGACTGCTG CAGTCTTGCCAGAATTTTCTTAAATACTGAGCTTCAACTTGGTCTGCTTGGT AATGGTATACCATAAGCCATGGACTTGATGCCCCTACAAAGCTCTGTGATTG AAATGGGATGCA	
25	<b>Rescue ID</b>	2C9E
	<b>Rescue Sequence 2</b>	
	CCCCGAACGCACTTTATATATATAAATATATATATTATTTTCTTCACTTATTTT CGTTTCGGCCGCGACAGCGAATATGCAATTTTCTCTCAATTGATTTTTTACA 30 CACTCGCACTCCTTTTACATGCGTGCAGTTTATGTTGCTATTGCTGCTACTGC TGCTGTTGTTGTTATTGTTGTTCTGGCTGCCGCTGCAGTGCAACTTGTAACACT TTCACATTTATGACATAATGCACTGGCCATATTTTGGCTTGGCTCTCCGTTTGT GCAACTGCATGTTCCCAGTGCTTTTTTAATATTTATGCTGCAGTGCGTGCAAAT TCGAACGCGAGACGATCCGCTTTTCGCTGCATCTATGCGCTGAAGATGTGCTG 35 CAGTCGATGGGCTCGTCGATAGTGGGAAGGCTCGGTGCCGGCACTATCGATT CCAACACCATAACGATAATATCGGCTAAAGTTATCAATATCGAAGTTTACTATA TTTCGGGTTTTTACGTTTTTAAATCTACCTTATCAACATTTTGNAGAAGTAAA AAGTAGTTCTCTTATGGATGCATC	
40	<b><i>Drosophila</i> EST</b>	several including LD10379 (AA816796)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	
	AE003733	CG3421 - novel protein with weak homology to myosin
45		

5	<b>Human homologue of Complete gene candidate</b>	Ensembl predicted Gene:ENSG00000071333 Clone:AC022505 Contig:AC022505.00011 5.60E-37 (predicted protein with Core domain in kinesin and myosin motors ENSG00000087179)
10	<b>Putative function</b>	Possible novel motor protein involved in cytoskeleton organization
	<b>Confirmation by RNAi</b>	Marked reduction of G1 and G2/M peaks indicating fewer cycling cells

**Example 6 (Category 1)**

**Line ID** 293/9  
**Category** Mitotic defects in brain: cytokinesis defect  
 5 (no overcondensation of diploids, very high polyploidy)  
**Reversion** NR  
**Map Position** 66B  
  
**Rescue ID** 2G5E  
 10 **Rescue Sequence**  
 GTACAAACGAATTATTTGTCTCCTTGTGCGTTCGTTTTATTGTGTTTCGAGTTCT  
 GTTGGTGTGTGTTTTTGTGTATGTTCCACGAGTTGTTTCGCATTAAAAAATTAAC  
 TGCAGAAGATCCATGGAAATGGAGACCATTGAAGAGCAATCGAAGTGCGGTG  
 AGTACTGAAAGAGGGCGCGGGGCGTGCGAGCTCCAAATGGCCGGCGAATTTA  
 15 TCATTTTCAATGTCGTCCAAAGGGGTTGGGTACGGGGTAAAACCACATTTCGG  
 GGCCAAAAGATCCTCATAAAAAATGTCGCTGCCAGCAAATGCAAAAAATAAA  
 ATAAAATAAGAACGACTATAAGTACATCTTTGTGTGTATTTGTGTGACTAAAA  
 AAGCAACGGCATCGTGTGCGCANATATTTTAATCTTTNTTTCTGAATTTATTTTCG  
 GTGTACAAAATATTTATCGCATAAATGCGAAATGCCTCCCTCTCTTCATCATCG  
 20 T

**Genomic hit, Accession No.** AC008303

**Associated ORF**

25 Genscan ORF1 predicted sequences >20:53:38|GENSCAN\_predicted\_peptide\_3|261\_aa  
 MMDNDDALLNNGGPQSGAETVYGTEDNNMVMSEKCRIFPATQRTGFVGATFSG  
 VLLLDLGALQHCDVIRIDVNIATLEQIKRERQEELAAERERIRAQIAADRAEQAQRF  
 NTPDISSTNSVAATAASNVTDDASVSSVDETRLQIRLPGGIQRKTSFPAGEVLAT  
 VRVYVRNEMLAASDVRDFTLATSYPREFQTEDEVKTLNELNLPNAVVLVLTK  
 30 EQVNPADDQTAKRSASTKRTKTHRHKRQLMADEPQSDHYKN

>20:53:38|GENSCAN\_predicted\_CDS\_3|786\_bp

atgatggacaacgatgatgcactgtcaacaatggaggaccacagtcggagctgaaactgtctacggtaccgaggacaacaac  
 atggatcatgtcggagaagtgcgcataatcccgcgactcagcgactgattgtggcgcgacgttttcgggagtgctgcttct  
 35 gatcttggtgccctccagcattgtgatgtatccggattgatgtaacattgcaacgctggaacagattaagcgtgagcgtcaggag  
 gagctggcgccaggagcgcattcgtgccaaattgcagccgatcggcgagcaggcacacgttttaatacggcgacat  
 tagcagcagaccaattcgggtggcgccaccgctgcctccaacgtgatcacacagacgcctcggtagtggtggagcagaga  
 cgaggctgcagatccgactaccggtggcattcagcgcaccaaatccttccagccggcgaggtgctggctaccgttcgtgtcta  
 cgtgcgaaacgagatgtggcgcgagcgtatgcgcactttaccctggctaccagttaccacgaaggaggtccaaacgg  
 40 aggacgaggtcaagaccctgaacgagcctaactagtgcctaatcggtggttctggtgctgaccaaggagcaagtgaatccag  
 ctgatgaccagacagcaaacgatcagcaagcacaacacacagacacacagcggaattgatggcagacga  
 gccacaatctgaccattataaaaactga

45 **Drosophila Gene Hit** rescue sequence: pebble (rho1 GTPase exchange factor)  
 (AF136492)

**Human Homologue** BLASTX with pebble: KIAA0337 (AB002335)

	<b><i>Drosophila</i> EST</b>	SD09146 (AI542703), SD01796 (AI530981)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003557
5	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8114 - pbl pebble rho1 GTPase exchange factor
10	<b>Human homologue of Complete gene candidate</b>	2224615 dbj BAA20795  (AB002335) KIAA0337 [Homo sapiens (3e-21 ) also mouse homologue 3e-95 42359 transforming protein (ect2) - mouse >gi 293332 (L11316) ect2 [Mus musculus]
15	<b>Putative function</b>	A guanyl-nucleotide exchange factor involved in signal transduction which is localised to the mitotic anaphase. pbl is required for the formation of the contractile ring and the initiation of cytokinesis in <i>Drosophila</i>
20	<b>Confirmation by RNAi</b>	Slightly reduced G1 and G2/M peaks indicating fewer cycling cells

- Line ID** 542/3  
**Category** Mitotic defects in brain: cytokinesis defect  
(very high polyploidy)  
**Reversion** NR  
5 **Map Position** 66A  
**Rescue ID** 2A1E  
**Rescue Sequence**  
GTCCAGTTAATGAAAGTAAACGAATCGAGTACAAACGAATTATTTGTCTCCTT  
GTGCGTTCGTTTTATTGTGTTTCGAGTTCTGTTGGTGTGTGTTTTGTGTATGTT  
10 CCACGAGTTGTTTCGCATTAAAAAATTAAGTGCAGAAGATCCATGGAAATGGA  
GACCATTGAAGAGCAATCGAAGTGCGGTGAGTACTGAAAGAGGGCGCGGGGC  
GTGGCAGCTCCAAATGGCCGGCGAATTTATCATTTTTCAATGTCGCCCCAAAGG  
GGTTGGGTACGGGGTAAAACACATTCCGGGGCCAAAAGATCCTCATAAAAAA  
TGTCGCTGCCAGCAAATGCAAAAAATAAAATGAAATAAGAACGACTATAAGT  
15 ACATCTTAGTGTGTATTTGTGTGACTAAAAAAGCAACGGCATCGTGTGCGCANA  
TATTTTAATCTTTTTTCTGAATTTATTTTCGNGTANAAAAATTTTATCGCATA  
AATGCGAAATGCCTCCCTCTCTTCATCATCGNTTCCCCTNACTCTCCCTCTCTT  
CGCCCGACACTGTACCGACGCAAGAAGAAC
- 20 **Genomic hit, Accession No.** CSC:AC018042  
**Drosophila EST** SD09146 ( AI542703), SD01796 (AI530981)

rest of results same as line 293/9

**Example 7 (Category 1)**

	<b>Line ID</b>	229/30
5	<b>Category</b>	Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects (Mitotic higher level of condensation, polyploidy, Meiotic:
	Ck05/07)	
	<b>Reversion</b>	?
10	<b>Map Position</b>	91F
	<b>Rescue ID</b>	A7E
	<b>Rescue Sequence</b>	TCTTGGCCAAACAACGCGAGCAGCTGATGTCGCATGGTGGGAAAATGAGGGT GGCGCGAGTGGAAGTTGCCATATCGCTGCGATCACAAGCAGCAAATATGGAA 15 GATTAAGCGGAAAACGAAAGACAAAATAATTACAATCAAACAACCGAATTAT AAAAAGAAAATGGTTTGTCTCCGAGTTCGTTTAAATATGCTTATCTACGTATC AATTAAAAAAACCGTAGAAAGAAATTCACGATTCACCCTAATCTAGCTAAGA CACCAACCAAAAATTTCCGATTTACTTTCAGTTGAAGTTGTTGTTACACACTTT TCTTGTCGATGTTTTGAAGCGCCCATTTGAAATTGATCATTGAAATGTTTTTCCA 20 AATTACCCACATCCATTACAATAAAATTTAAATTGCTTATTATTTGATTTTTACT TGGGAAAATCCCCTTGCCAAATTGGAATTACAATTCCAGCTTGGAATCCGTCA AACTTTACAACATAAACTTATTGTTCTTTTCCGGACAATGCTTCCA
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003686
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG6284 - novel protein possible sir2 family of transcriptional regulators/telomeric silencing
30	<b>Human homologue of Complete gene candidate</b>	gi7706710 0268A424791DE5BF [ref]NP_057623.1  sir2-related protein type 6 [Homo sapiens] (1.10E-74)
35	<b>Putative function</b>	Putative transcriptional regulator
40	<b>Confirmation by RNAi</b>	Complete loss of G1 and G2/M peaks indicating fewer cycling cells

	<b>Line ID</b>	1104/16
	<b>Category</b>	Mitotic defects in brain, Cytokinesis defect (no overcondensation of diploids, high polyploidy)
	<b>Reversion</b>	R
5	<b>Map Position</b>	92A
	<b>Rescue ID</b>	B5E
	<b>Rescue Sequence</b>	GTCCGGAGCGGAGCTAAAGTTCGATGTTTCGTGCAAAACACTTCGATTCCGATA 10 GGCGGATGCTATCGATTTTCGGCGATGCCCGTTGGTCACACTTGGTGGTGGGCG CTGCCCCGTCGCCGACTATCGATAGCACAAGCGGGTTATTTAGGTGTGCGCAGC TTGTAAGGGTGACTCATGCTGTTAAAATTATTATAAAAAAGTTAATGAATATAA TATAGTTATAATAAAATTATATATAAATCTATAAGATCAAAGATCATCAGTTA TCATTTATCATTTGATTATATGAAAAACAAGAACAGAAACAAGATTTAATAGG 15 TTTTGTGAAATGTGAAAATGTGGGTTACCCCCAATTCTTATTCGAAATTAAATAA CCTAAAGAACAGTTATACACAGATAGGTAATTTGCACATAAGCCAAATTTGT CTAGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCCGTGATACGCC TATTTTATAGGTTAATGTCATGATAATAATGGTTTCTTA
20	<b>Rescue ID</b>	B5P
	<b>Rescue Sequence</b>	CTCCGGACACGCAGTAGCTAAATAACAAACTCATTACTAGTATATTACTGCCG CCGATTTGCAAGCGCGTACCGATCCCGATACCAGGCCAATCGCACTCCCCAGT TGTACGTCATCACTTAAGTAATAAATCAGCGGCAAATCGCATAAATTGCTATT 25 GATATTCCGCCCGCTGTGTGTGCGTGTGTATTTGCAAGAGAGTGTGTGTGTGT GTGTGCATATGACTCGTGCGTTTAGCCGACAATTGGAGAAAAAGCATTACCAA TCCCAATTGGCTAACTAACTAAAGTTGGCTTGGCCAAACATAAACAAGT GCGGGCGCAGCGATTTGGCAGCGAAACATATACACCAAAGCGCTATTGGCAG ATATATATGTAGATTAAATATAGAAAGTGCGTGCGAAGGTTAAGAGTCGAGT 30 GCAAGTGCATTTATATTTGGAAATAATAAATGCTACAAT

other results same as 229/30

**Example 8 (Category 1)**

**Line ID** 343/5  
**Category** Mitotic defects in brain: cytokinesis defect  
(very high polyploidy, chromosomes entangled?)  
**Reversion** NR  
**Map Position** 75B

**Rescue ID** C6E

**Rescue Sequence**

GGTTTCGAGTTCGTTTCGGCTCTCCGTTTCGGCTCTCTCTCGCCATCCC  
GCTGCCGCACACATTGGCCTCTCTCTCGCAGCTCCACATTCTGAAGGTGGCTGA  
CCGAAATGTGGGTCACGACAATGGCGGGGTTTCGTTGAACTGAACCACCGCCG  
CAGTCGCTGCCGTGCTCGCTGCTCTGCCTCTGCTGACGTCGTTAACGTTTTGGG  
GCTTTCGGTTACGTAGCTCGTGTGCGAGCGAGAGGGGCTACTAGAGGGACTGC  
GACACACAAGTTGTGTGCATTTTTTGGCCCCAAAAAATCACAATGGGCACAAA  
ATATTATTTAATACATCACATAATTGTTTAAATCATCTGGCTGGAAAGTGTCTGAG  
TTCATCGAACTGCCAGCGATTGACAAATTGCGATTTTCAATGCGGCAAAAATA  
TTTACTCAAGCAAATTGTTTGCACCTCGTTAATTAGGCGGGGAGTGCCGCCAA  
ATTGGGTCATATTGCAGAAAGTATCCAAGAAGTTGGAGAAACAAGCTGCTTAA  
ACATTAATTAACACACACCTAAATGGATACATTTGCTACAAACAATTATAAAT  
GTTACCCTTATATTAATTTTCAAATTTCTAAATAATCAA

**Genomic hit, Accession No.** CSC:AC015427

**Associated ORF**  
Genscan ORF1 predicted sequences  
MVCAMQEVAAVQHQQQQQQLQLPQQQQQQQQTQQQHATTIVLLTGNGGGNL  
HIVATPQQHQPMHQLHHQHQQHQQHQQQAKSQQLKQQHSALVKLLESAPIKQQ  
QQTPKQIVYLQQQQQQPQRKRLKNEAAIVQQQQQTPATLVKTTTTSNSNSNNTQT  
TNSISQQQQQHQIVLQHQQPAAAATPKPCADLSAKNDSSESGIDEDSPNSDEDCPN  
ANPAGTSLEDSSYEYQCPWKKIRYARELKQRELEQQQTGGSSNAQQQVEAKPA  
AIPTSNIKQLHCDSPFSAQTHKEIANLLRQQSQQQQVVATQQQQQQQQQHQQHQQ  
QRRDSSDSNCSLMSNSSNSAGNCCTCNAGDDQQLEEMDEAHDSGCDDELCEQH  
HQRLDSSQLNYLCQKFDEKLDTALSNSSANTGRNTPAVTANEDADGFFRRSIQKQ  
IQYRPCTKNQQCSILRINRNRQYCRLKKCIAVGMSRDVLRLEQPKAGAKNKSCE  
PSKNSTVNQINSKLELGNSNEMK

>21:55:09|GENSCAN\_predicted\_CDS\_1|1533\_bp

atggttttgcaatgcaagaggtgctgccgtgcagcatcagcagcagcaacagcaactccagttgccccagcagcaacagcag  
cagcagcagacaacacagcagcaacatgcaacaactatagtgctgctgacgggcaatggcgcggtaatctgcacattgtcgcc  
acaccgcaacagcatcagccgatgcatcagctccaccatcagcatcagcatcagcaccagcagcagcccaagagcc  
aacagctgaagcaacaacactcggcgctggtcaagttgctggagtcggcgcccatcaagcagcaacagcagacgccaagca  
aattgtttacctgcagcagcagcagcagcaaccgcaacgcaaaaagactgaaaaacgaagcagcaatctacaacagcaacaac  
aaacacctgcaacactagtaaagacaacaaccaccagcaacagcaacagcaacaacacccagacaacaatagtattagtcag  
cagcaacagcagcatcagattgtgtgagcagcaccagcagccagccggcgagcaacaccaagccatgtgccgatctgagcg



ccaaaaatgacagcgagtcgggcatcgacgaggactcccccaacagcgatgaggattgccccaatgccaacccggcgggcac  
 atcgctcgaggacagcagctacgagcagtatcagtgccctggaagaagatacgctatcgcggtgagctcaagcagcgcgagt  
 tggagcagcagcagaccaccggaggcagcaacgcgcagcagcaagtcgaggcgaagccagctgcaataccaccagcaac  
 atcaagcagctgcaactgtgatagtccttttcggcgagaccacaaagaaatcgcaatctcctgcgccaacagctccagcaac  
 5 aacagggttggtggccacgcagcagcagcagcaacagcagcagcagcaccagcaccagcaacaacgaaggatagctccgaca  
 gcaactgctcgtgatgagcaactcgagcaactccagtcgggcaattgtgcacctgcaacgctggcgacgaccagcagctgg  
 aggagatggacgagggcccacgattcgggctgcgacgatgaacttgcgagcagcatcaccagcgactggactctcccaactg  
 aattacctgtgccagaagttcgatgagaactggacacggcgctgagcaacagcagcgccaacacggggagggaacacgccag  
 ctgtaacagtaacgaagatgccgatggattcttcgcccgtccatccagcaaaagatccagtatcgcccgtcaccaagaatca  
 10 gcagtcgagcattctgcgcatcaatcgcaatcgttgtaattgccgcctgaaaagtgcattgccgtgggcatgagtcgcatgt  
 tctgcgcctagagcaacctaagctggtgccaataaagtcattgtgaaccgagcaaaaattcgaccgtcaaccaataaacagc  
 aaactcgaactcggaacagcaatgaaatgaaatga

***Drosophila* Gene Hit** TBLASTN with ORF1: ecdysone-inducible gene E75B (X51549)  
 15 and nuclear receptor superfamily protein (U01087) BLASTN with  
 genomic sequence matches ecdysone inducible gene

**Annotated *Drosophila* genome genomic segment** AE003522  
**Annotated *Drosophila* genome Complete gene candidate** CG8127 Eip75B ecdysone-  
 20 inducible gene E75B nuclear  
 receptor NR1D3

**Human homologue of Complete gene candidate** ORPHAN NUCLEAR  
 25 RECEPTOR NR1D1 (V-  
 ERBA RELATED PROTEIN  
 EAR-1) (REV-ERBA-  
 ALPHA) Q15304 (9.40E-74)

**Putative function** Ligand-dependent nuclear receptor, putative transcription factor  
 30

**Confirmation by RNAi** Slightly reduced G1 and G2/M indicating fewer cycling  
 cells

35

	<b>Line ID</b>	448/23
	<b>Category</b>	Mitotic defects in brain: cytokinesis defect (very high polyploidy
	<b>Reversion</b>	NR
5	<b>Map Position</b>	75B
	<b>Rescue ID</b>	2G4E
	<b>Rescue Sequence</b>	
10		GCTGGTGGACGCTGCTTTCATTTCGCAAATTGCTCGTCGTTGGCAGCGGTTGTGC AGAGCAAGAAAAGCGCGCGAAAAACCAAGCAAAAAATTAATACAGCTGGAT CAAGCGAAAAGAGATAGAGAGCAGAGTCAACAGCAACAAATGTTCAATAGCA AATGATATCGCATATTTTTGTTGGTGCCAGTGAAGTGAGATCAAAGTGAAGTG TGCAATGTTCTTATTAGCAAATCGTAGAGCAACCAACAATCGAGAGTTCAAG TGTCATTTTGAAGCCAAAAAGCAAAATCTCTAATTCAAATATGGTTTGTGCAA 15 TGCAAGAGGTTGCTGCTGTGCAGCATCAGCAGCAGCAACAGCAACTCCAGTT GCCCCAGCAGCAACAGCAGCAGCAGCAGACAACACAGCAGCAACATGCAAC AACGATAGTGCTGCTGACGGGCAATGGCGGCGGTAATCTGCACATTGTCGCCA CACCGCAACAGCATCAGCCGATGCATCAGCTCCACCATCAGCATCAGCATCAG CATCAGCACCAGCAGCAGGCCAAGAGCCAACAGCTGAAGCAACAACACTCGG 20 CGCTGGTCAAGTTGCTGGAGTCGGCGCCCATCAAGCAGCAACAGCAGACGCC CAAGCAAATTGGTTACCTGCAGCAGCAGCAGCAGCAACCGCAACGCAAAAGA CTGAAAAACGAAGCACAATCGTACAACAGCAACAACAAACACCTGCAACAC
	<b>Genomic hit, Accession No.</b>	CSC:AC015427
25	<b>Drosophila EST</b>	GM03519 (A801874)

Other results same as line 343/5

**Example 9 (Category 1)**

5	<b>Line ID</b> 36/1 <b>Category</b> Meiotic defects in testis: cytokinesis defects (Ck-04/06) ` <b>Reversion</b> R <b>Map Position</b> 79C
10	<b>Rescue ID</b> A8B <b>Rescue Sequence</b> GAGTAAAGTAAACTACAGAGAAAAAACGCTTTACGGCGAGAGAACGCTTTAA TTATACTTAATTTGTTGTTAATCAAACGCACAGAGCACACAACACAGAAACAC AAAACACCGCTTGGGAAAAATCTGTAGGTAGANGAAAGGAGCTCACGTTTTT CTGGTGCAGATCGAAATCGGTATCGGGTTTATTTCGCTTTGCCGGATTGTTACTT 15 CACGTTTGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCGCACACTTTGATTT GCGTTTGCAACTCGCAATTCGCAATTGGCATTGCTATGCGACAACGCGGTT ATTTCCGGTCCGTTTACTTTTCCAATGGCTTGCCTACACACCGCCAAACTTTGG CTTGAACCTGGGATATTGGTTGCCCGAATTTCTTGANAAATTTTCCTT
20	<b>Genomic hit, Accession No.</b> CSC:AC013886
25	<b>Associated ORF</b> Genscan partial ORF1: >18:33:59 GENSCAN_predicted_peptide_1 99_aa CICFALLGLLIRKLMVVFGSTSRKAQSLESRRAKNTSQKIGNQYPKFSQVCGKPS KSNDRNNGSCRANANCELRVANANQSVRRRIRNKETQLTNVK  >18:33:59 GENSCAN_predicted_CDS_1 300_bp tgtatctgcttcgccctgcttgggtactcattcgcgaaaaattaatgggtggtgttcggttctacgtcgcgcaaggcacagtcctctaga gtctcgagagctaagaatacatctcagaaaatcgcgcaaccaatccccaggtcagccaagttgcgcgcaagccatcgaaaagt 30 aacgaccgaaataacggcagttgtcgcatagcaaatgccaattgcgaattgcgagttgcaaacgcaaatcaaatgtgctgcagg agaataaagaacaaagaaacgcaattaacaacgtgaagtaa
35	<b>Drosophila Gene Hit</b> rescue sequence and TBLASTN with ORF1: nucleic acid binding protein (mub) (X99340) <b>Human Homologue</b> BLASTX with nucleic acid binding protein: poly(rC)-binding protein 2 (hnRNP-E1) (S42471) <b>Drosophila EST</b> several including LD32520 (AA951799 BLASTN matches nucleic acid binding protein (X99340)
40	<b>Annotated Drosophila genome genomic segment</b> AE003596 <b>Annotated Drosophila genome Complete gene candidate</b> CG7437 - mub mushroom bodies RNA binding protein
45	<b>Human homologue of Complete gene candidate</b> 4826886 ref NP_005007.1 pPCBP2  poly(rC)-binding protein 2

79

>gi|542853|pir||S42471 (4e-75)

5    **Putative function**    A putative RNA-binding protein specifically expressed in the CNS of *Drosophila melanogaster*

10    **Confirmation by RNAi**    Only wild type profiles observed

**Line ID** 472/22  
**Category** Female sterile  
 (anaphase bridges, lagging chromosomes)  
**Reversion** ?  
 5 **Map Position** nd  
**Rescue ID** sau 5'spl

**Rescue Sequence**

10 GCACGATCNCTAAAGTCTNGCANAGCTAAAAATACATCTNAGAAAATCGGCA  
 ACCAATATCCCAAGTTCAGCCAAGTTTGCGGTGTGTAGGCAAGCCATCGAAAA  
 GTAACGACCGAAATAACGGCAGTTGTGCGCATAGCAAATGCCAATTGCGAATT  
 GCGAGTTGCAAACGCAAATCAAAGTGTGCGCAGGAGAATAAGAAACAAAGA  
 AACGCAATTAACAAACGTGAAGTAACAATCCGGCAAAGCGAATAAACCCGAT  
 15 ACCGATTTTCGATCGGTGCGGGCCTCTTCGNTATTACGCCAGNTGGCGAAAGGG  
 GGATGTGCTGCAAGGCGATTAAAGTTGGGTAAACGCCAGGGTTTTCCAGTCACG  
 ACGTTGTAAAACGACGGCC  
 ANTGCCAAGCTCTGCTGCTCTAAACGACGCATTTTCGTA CTCAAAGTACGAAT  
 TTTTCCCTCAAGCTCTTATTTTCATTAAACAATGAACAGGACCTAACGCCNGT  
 20 AAC

**Rescue ID** Sau 5'splac

**Rescue sequence**

25 GTTGTGATCNTCTTGGTNAATCNNNTTGGAAAATCCCCTAANGCTTCCGACAA  
 TGACCCNGNCNTACNNAGCAAANAATNGNAGNACNNGCNGNTGGNCGTANT  
 ANCAANAACAGGCCCGCACCGATCGAAATNGGNATCGGNTTTATTCGCTTTGC  
 CGGATTGTTACTTCACGTTNGTTAATTGCGTTTCTTTGTTTCTTATTCTCCTGCG  
 CACACTTTGATTGCGTTTGCAACTCGCAATTCGCAATTGGCATTGCTATGCGA  
 30 CAACTGCCGTTATTTTCGGTCGTTACTTTTCGATGGCTTGCCTACACACCGCAA  
 CTTGGCTGAAC TTGGGATATTGGTTGCCGATTTTCTGAGATGTATTCTTAGCTC  
 TCGGAGACTCTAGAGACTGTGC

Other results same as line 36/1

35

**Example 10 (Category 1)**

	<b>Line ID</b>	459/2
5	<b>Category</b>	Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defects: (mitotic: high polyploidy, no diploids, higher mitotic index, meiotic: Ck-01/05)
	<b>Reversion</b>	NR
10	<b>Map Position</b>	66B1-6
	<b>Rescue ID</b>	2D5P
	<b>Rescue Sequence</b>	GCTCCGTTTCGAAAAGTTGAGAGAGACTTGAAACATATGTTTCGGCGTTGCTAGAG CTGGTCGGCTACCGATAGAAACATCGATAGGTCCGATGTTTTTACTCGTATAT 15 TGATTCANAGTTTGGCTATCGATGTTTTTAGAGTGCCCGCACATTATCTATTTT CATCTCTATTTTCGTTGGTATTTTTTGTATTTTATGACATTTTCGACTGCAAAAGC AGGATGGCAACGCCAGATTGCCGCGAAAAGTACGTTATTTTTAAATTGGCGCAT TGAATATGAAAAATTGCAGGCACATACAGTTTCTAATAAATAATAGCAATAAT TATTATTTAGCTTGTATCATAACGAAGTGCACATTACAGCTACGCATCTGAAAT 20 AATAATTTTAATATATCGTCTTTTCTCCCATCGATAGAGTTCGCGCCTATCGA TATATCGTTGATCACCAAATAAATAAACTAAATAACGCCGCAATGGAACAC GCGACGAGTGAATTGAGGGAATTTATCTCAGATCTTGTAATTCCGCACCCACGT TGCAATGGTAACATCAATCCGGATCACATCACAATGCTGGAAGGCACCCAGA TCCAGAACAG 25
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003557
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8038 - novel gene ribonuclease P homology 30 CG7892 nmo - protein serine/threonine kinase involved in eye morphogenesis
35	<b>Human homologue of Complete gene candidate</b>	CG8038- 5e-24 4309676 gb AAD00893  (AF001176) ribonuclease P protein subunit p29 [Homo sapiens/]
40		CG7892- protein kinase mitogen-activated 7 (MAP kinase)' gi:4506093 and gi:7706445 D919050533B3C33A
45		[ref NP_057315.1 ] nemo-like

kinase [Homo sapiens]  
(3.30E-174)

- 5    **Putative function**    CG8038: tRNA processing enzyme Ribonuclease P protein subunit  
CG7892: a protein serine/threonine kinase involved in cell cycle,  
possibly targeted to cytoskeleton

- 10    **Confirmation by RNAi** Both showed a marked increase in G1 peak indicating arrest in  
G1

**Example 11 (Category 1)**

	<b>Line ID</b>	623/8
5	<b>Category</b>	Meiotic defects in testis: cytokinesis defects
	<b>Reversion</b>	?
	<b>Map Position</b>	37E1-3
	<b>Rescue ID</b>	2E2E
10	<b>Rescue Sequence</b>	
		CTACGGGCATTTCGCATGTTTCGAACATCTGGTGTAACAAGTTCTGAGCAGTGT TGCCAACTCTTCAGTTAAACAGTTAAAAATAGCTAAAAAATGTTGACGGTAGC TAAATTATAAAGCTAGAAAAGAAATGATATATGATAAAATAAGTATTTCTGACT CACAGCATTTATTATTTAAGACGGTCAGATGAAGTTACAAAAATCCTAAATTG 15 GCGCGCTGTATCTAAGAATTAATACCAAGAAGTTGTCATCAAAGGTCGAACTC GACGGAAATTCTACTTTGAGTTTTTAAATTTAATAAATATGTATTTAAATTAT GTAAATTTGTTTGTAACAAAAATAGTATATAGTATAGTAATAGTAGTTAAG TAGTTTTAAAAATGGCCAGATCAAAGACTTTTGAGATATGATACTAATCAAAA GTCGAATTCGCGGAATTAATTCTTGAAGACGAAAGGCCTCGTGATCGCCTATT 20 TTTATAGGTAATGTCATGATAATAATGGTTTCTTAGACGCAGGTGGACTTTTCG GGGAAATGTGCGCGGAACCCCTATTGTTATTTTCTAAATACATTCAAATATGT ATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGG AAGAGTATGAGTATTCAACATTTCCGGGCGCCTTATTCCTTTTTTGGGCGGCAT TTGCCTTCCTGTTTTTGTACCCAGAACGCTGGTGAAAGAAAAGATCTGAAGA 25 CAGT
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003662
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG17559 dnt - doughnut protein tyrosine kinase
30	<b>Human homologue of Complete gene candidate</b>	Homo sapiens RYKreceptor tyrosine kinase GDB:21773
35	<b>Putative function</b>	growth factor transmembrane receptor protein tyrosine kinase involved in cell growth and maintenance
	<b>Confirmation by RNAi</b>	Only wild type profiles observed



**Example 12 (Category 1)**

	<b>Line ID</b>	629/14
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects (Ck-06/09)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	64D
	<b>Rescue ID</b>	2A9X
10	<b>Rescue Sequence 1</b>	
	GACGGGAGGAAGTAAGTGGGAGGAGAGAGTAGTGCCTCTTTTTTACTGGAGA AATGGACAAACTCTGGGAACTGCGAACTGCGAACTAACCGAGGCAAAAATTG AGAAGCGAGCTGAAAGCGGAATTCAAACAACGCAGCGCTGACGGCGACGCCG GCAGAAGCAGCGCCGCACAAGGCATGCGCACAGAGAGTAAGAAAGAGCGCG 15 GCTAATGAATGAATGAACGAGGCGGAATGCGGGAAGAGCGCAGAGAGGCGC AATGACAAAATAGTTGTAGAAAAGCGCCGGCAAGCGGAACTCCACACTCTTT CTCACTCTCTCTTTCCACCCACACCCCTAGTTCACCGGAAAAAGAAAATTTCGTT TGCGGCGGGGGTGTATTTTACCAAAAAGAGAGTGTGTGCAAAACGCTAGA GAGAGAGAGAGAGAGAGAAAGAACTGACGTGAGTTCTGCCTCCGTCGACGCC 20 GCTGCCGCGCTCCCAAAGCGCCACCACCCAAAAAACGCGAGAAGAAGCAGA ACAAACACACACAAAAATTCGCACAGTGGAGCAGAAATCAAGC	
	<b>Rescue ID</b>	2A9E
25	<b>Rescue Sequence 2</b>	
	CTCCCGTCGTTTTGAGATCAGCTGCTCTCGCAACAACAACAACTATAACTGTA GTTACCGTCTCTTTTGCATCGTTTCGTTTTTCGTTTGTGTCGCCAAGTGATTGTGT GTGTGCGTAAGCTTAAAGCTGACTAACAAAACGAAACAAGAAAAAATATAAA TTATAGGAAAATTGTTAAATTATAACCAGAAAAGAGAGCGGCACCTTACGTGTGT TATTGTGTGCGTGTGCTTTAAAAAGATATAAAAAATAGCAATAGAAAAGTTATTA 30 AAGCGTTGGCAAAAAAGTCCAACGAACAGCGAGAGGAAGCGGAGAACGAAA TAGTTAAAGCCAAAGTCGCTGCCGACGTCGCACTTGAAAACGTCGCAAAAGTT TGTAACACACACAGTGTGTGTTTCGTGTGTGTTTTTGCCGGCGTGCCAGTGTGCG TGCGCCTAGAAAAGAGTAAAGAAGCAGAAGAAAAGGAAGAAGCCGAAGAAG CAGCAAAAGAAGCCGACAGCAAAAAGTAAATAAAATCAAATGCCCCCTGGCA 35 GAATAATATTAAATTAAGACACATACTCAAATTAATAAC	
	<b>Genomic hit, Accession No.</b> CSC:AC015076	
40	<b><i>Drosophila</i> EST</b>	LP08767 (AI295205)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	
	AE003567 CG10668 - novel with homology to ssDNA/RNA binding proteins	
45	<b>Human homologue of Complete gene candidate</b>	
	CG10668 - 3e-12 4506449	

ref|NP\_002889.1|pRBMS2|  
RNA binding motif, single  
stranded interacting protein 2  
>gi|1082

5

**Putative function**      Possible single stranded DNA/RNA binding protein

**Confirmation by RNAi**      Slightly increased G1 and reduced G2/M indicating G1  
10    arrest

### Example 13 (Category 1)

5	<b>Line ID</b>	653/12
	<b>Category</b>	Meiotic defects in testis: segregation defects, cytokinesis defect (Ck-07/35)
	<b>Reversion</b>	NR
	<b>Map Position</b>	75B
10	<b>Rescue ID</b>	I5E
	<b>Rescue Sequence</b>	GTAAAAGCTTAGCCCATGGCGTCGACGTCGACTGCGACAGCGACGCTAGCCG AGGCAGTGACTGCGACGTTGGCCACTTTTCGCCTTCGTTTCGCTGTCGTTTTCA GTTGTCTCTCGTTGCTCAAAGCGCGCGGCACGCGAACGCTCTGAAATCCCAAG TTACAACAGCAACATCAAGCAGCAGCAACAACAGTGATTCGCTGGCAAACAA 15 ACAAACAAACCAACATATTTTTGTGTATCAATTGTCGGCCTAAAACCTTCACAT AAAAGTGCGTTCAATACGAAACAAATATATTTGTATATATAGAGAGCGAAGC AATCGGTTGCATAAATTGAATTCGGTTCATATACTTCAATATAAATATTATTAA GTACTACAATTTGAAAACATCTTTAAATATACAACATATTTTGAATTAAGTTTA TTTTTTTTTTTTAGCCACATAGAGACATCTTTGTGGCATGCTAAATTCTGTAGTA 20 AAACCTTCTTGGGGAAAGTGAAAGCCACGTATCAGACCAAAATCCACCCAAC CCTGCACACACGCATCCCCATAAAGAACGACCTTGAGCT

**Genomic hit, Accession No. CSC:AC014071**

25 **Associated ORF**  
Genscan ORF1 predicted sequences >16:36:33|GENSCAN\_predicted\_peptide\_2|477\_aa  
MLILMRPSIKLAANQNAIKAPNGPKNFLDKVLVVRCSLVCLENGHIAVTASGS  
NNNNNSNNINLNLKANYQMSATSIRDSFATILLDAQNRVQNATVAAKNFMLPLR  
LRSDTSGDTSNNNENNSRRARQAYNCGVNWLTTHRPKRRRQVHPPLGSTPSCNN  
30 NSSKISRNSSSSNNIASATATRIFLGTSAILAIDFDNTRVPGYYQPTGEWIWVSKS  
MIKQLFAVAATADDVAAAAASRGNALTFPGKEKGPRKKAEGCGMEWSGVIEWS  
GGDVMCVLSSVATVDDDDHHGGGHFDGLLGTPSALIRLNCLINPKKMRMDFEVE  
VAWQIARAADRLISMHLNVPIYEMKTMKTMSVIDGGSLYQPTALFGSLFCLVY  
SSAADVLLLLANCKSLAHGVDVDCDSASRGSDCDVGHFSPSFRCRFQLSLVAQS  
35 ARHANALKSQVTTATSSSSNNSDSLANKQTNQHFVYQLSA

[illegible]

ggaaaaagcgcggaagggtgtggaatggagtgagtgaggatggagtggtggcgatgtgatgtgtgtctctcagatgtg  
gccacagttgacgatgatgatcatcatggtggcgccacttgcagcgctgttgggaacaccttcagcgctcatccgacttaactgc  
ttaatcaaccggaagaagatgaggatggacttggagttgagttgcatggcaaatgtctgagctgctgatctcggtgatctca  
atgcaccttaatgtgccttatgaaatgaaaacgatgaagacgatggagagcgtgatcgatggtggctccctgtaccaaccgactgc  
5 tctctcggttcitgtttgttggctgtattcttcagctgctgatgtgtgttgtgctgctggcaactgtaaaagcttagcccatggcgctg  
acgtcgactgcgacagcgacgctagccgaggcagtgactgcgacgttggccacttttcgcttcgttgcgtgctgtttcagttgtc  
tctcgttgcctaaagcgcgcgggcacgcgaacgctctgaaatccaaagtacaacagcaacatcaagcagcagcaacaacagtga  
ttcgctggcaacaacaacaacaacaacatattttgtgtatcaattgtcggcctaa

- |    |   |   |
|----|---|---|
| 10 | <b><i>Drosophila</i> Gene Hit</b>                                 | rescue sequence, ORF1 and genomic sequence: Canton S E78B nuclear receptor superfamily protein (U01088)   |
|    | <b><i>Drosophila</i> EST</b>                                      | LP11082 (AI296953 similar by BLASTN to U01088)  |
|    | <b>Annotated <i>Drosophila</i> genome genomic segment</b>         | AE003593  |
| 15 | <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b> | CG18023 - Eip78C<br>Ecdysone-induced protein 78C<br>nuclear receptor NR1E1                                |
| 20 | <b>Human homologue of Complete gene candidate</b>                 | CG18023- 4e-32 119100<br>P20393 EAR1_HUMAN V-<br>ERBA RELATED PROTEIN<br>EAR-1<br>>gi 1082832 pir  A32608 |
| 25 | <b>Putative function</b>  | ligand-dependent nuclear receptor , putative transcription factor   |
|    | <b>Confirmation by RNAi</b>                                       | Not done due to failure of PCR procedure  |

**Example 14 (Category 1)**

	<b>Line ID</b>	876/2
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects
5	<b>Reversion</b>	?
	<b>Map Position</b>	73A
	<b>Rescue ID</b>	2H1E
	<b>Rescue Sequence</b>	
10	GATCAAACAGAAAATCCAAAAACGAACAGCGCGCGGCGAACGAGAGCCGTT	
	GAAGCCCGGCAGAGAAGTGCGCTGCTCGCGTCGCTGCCGGTATGTGCGTGTCTG	
	TGCACTGAGAGAAAATGCTCGATTAAACAGAGAAATTAATAGTAATATAAAA	
	AAAAAAAAAATTTGTTTATTATTCTCAATTCAATAAAATGTAATTATTTATTAT	
	ATTGGTTGTATAAGAATTTTTATAAAGTAGTATAAAATTTCAATCAAATAAAT	
15	ATGTACATCTAACAAAAAATGTTATTATCTTATAACAAAGAGGTAAAATCATA	
	AGTAGTACGAAATCTTTAAAAGAGAAAGTGTTACGCAAAAAGTATTCAAA	
	GCAGTCTTTTATTTAATTTAATTAATTTATTTGTGCTTTATCCCTTATATATATA	
	TGTACATTTTCATTAAAGCTAATGGTATAATTAGGTATTTACAGTGTTTAGCTAA	
	GGCTTTTCATCTGAAATATTTATTAATTATGTCTAGTTGACCTGTTTTTAGTTTTT	
20	TTGNATAACAATATTTATTATTTATTAAGGAAAACAAGGGGAGAAGAAAAAC	
	CTTAATTGAAGCAAAGCAGTCTTTTGAACCCACTGGTG	
	<b>Genomic hit, Accession No.</b> AC005633	
	<b>Drosophila Gene Hit</b> rescue sequence: argos (M91381)	
25		
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003527
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG10162 – Egf2 translation facto
30	<b>Human homologue of Complete gene candidate</b>	CG10162 - 4e-11 181969 (M19997) elongation factor 2 [Homo sapiens]
	<b>Putative function</b>	Translation elongation factor
35		
	<b>Confirmation by RNAi</b>	Not done due to failure of PCR procedure

**CATEGORY 2: FAILURE TO ENTER M-PHASE****Example 15 (Category 2)**

	<b>Line ID</b>	1216/12
5	<b>Category</b>	Meiotic defects in testis: no division (no meiosis)
	<b>Reversion</b>	NR
	<b>Map Position</b>	82F1-2
10	<b>Rescue ID</b>	2I5X-1
	<b>Rescue Sequence 1</b>	AAACCAAGCAACAGAAATATCTCCAGTAGAGAGCGCCACTGGAAGATCGGAA TTTTAGTGCTCTGCTCTGACTAACAGGTTTTAGTAGTAGTGCTTACTTTCTAC TACGATTTTTGTGCGCGGCTAACAAATCTGTTTTCCCACTCCCTCTCTCAGTTTTT 15 GCATGGTAACCTTTTCGGTCATTGTACTGTTGTTGTTGTCTTGCACACCGCAAGA GAACAACAACAATCGGAGAAACACTGATAGCGCGGTACAGTGGGGCAGGCCA AACTAGAACCTATACATTTAAGATGTCTCCAATTTGTGATTTTGCCTTTCAAGC ATACTAGTTCATAGTTGATTGTTTTGTTATGTTTTGTCTTGAATGCGATGTTTCA AGAAATCTTATTTTCGAATTACGATATTATTCTTATTCCTTTGACTTATTAAAA 20 TAAATGAAAACGGCGAGTAGAGCAAAAGAGCGACCACTGTGGCTCCACAAGC TCGTTTCTCTGTTTCTCATTGCGGCCAGCTCCAATTTGCCTTATTCACACACA CACCTCACTGCTTGCGACTGCAAATTTGTGCAGCTGAACTTTG
	<b>Rescue ID</b>	2I5E-1
25	<b>Rescue Sequence 2</b>	CTTGGTTTATCACCTCTCTCTCTCTATCGCGCGCGCGCTCTTTGTGGAA ACAGGTATAACTGTTTGGCGTGAGGGAGCACGAAACTCCAGTGGAGACTTCTC CGCATCGCCAGCGAAACAAACGATCAAAATGAATACTCTGATAACGTGTGAA GGTGAGCAACAAAATAAAGTATAAGAAAAATACCGCCACGAAAACAACAACA 30 ATAGAAATGTCGACGCACCTTTTCTTTTCTCGCAAAGAACGAGGAAATGGA GAAGCGCAAAACCACATCCCGCTTAAAGAGTCCCTTTCCCCCGCTGGAAGTGG AAGGAAAGGCAGCTTAAAGAGGAGCGGGTGGCTTCCAGTATGTGGAAAACAA AGCAGACGCCATTGGAATGCCGTCGTTTTTGTGTTGCTAAGCCGGACATGG CAATTGTTGCTTTTGTTCGAGAGGGGGTGGTGAAACTCATAAATATCAGCT 35 ATGGCGAGGGGGTGGGGGCAGTCTTTGTCTGACGTACCGTACTTTTAATTTCTT GTCGCCCGGTTTAATCCAATTTATCCAGCTTTGAATTTGCGCG
	<b>Genomic hit, Accession No. AC007532</b>	
40	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003603
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate CG1116 - novel</b>	
	<b>Human homologue of Complete gene candidate</b>	2495728 HYPOTHETICAL PROTEIN KLAA0258(aa)

**Putative function**      No homologies which indicate function

**Confirmation by RNAi**      Slight loss of G1 peak

**Example 16 (Category 2)**

	<b>Line ID</b>	1344/15
	<b>Category</b>	Mitotic defects in brain: no mitosis
5	<b>Reversion</b>	NR
	<b>Map Position</b>	83C
	<b>Rescue ID</b>	2F6E
	<b>Rescue Sequence</b>	
10	AGCGGGAGTGAGCCGAAAGAGAGTAATTTGGCCGTCACCAAAAAAGTGGCT GCATAGTGCCAAACCAATGTATGGCCGTTACGCATCTTGTTATTCTAGTGTCTT TGGCTGTAATCAGTTTGCAGTGACAGAGGAGTTCAGTTTCAGTTGACTCGGCT TGGTTCAGGGTTTCTGATTGCCGTCCTCTTCTCCCTCTTCGCCTACAAGTCCGC TGTTCCGGCACCGTGACGTCACCTAGACTTACACCCCTAATCAAAGATCCACTA 15 GTTTAGATTTTCCTGCATCAACGCCATATTAACCTTTATAAGCAGTCGTTATATCT CAAGTAGGCCAAAAAGTGTAATAGATATGTATCTAAATTGTCGTACATTCTAT TTATTAATAATTCGTTTTTACATCCAACAGGTGTTATTTTTGAAGTCTTAGATAA CAAACAATATTCGAATTATGTGGTAGAATACTTAGCAATATACGCACATACAT ATACATATGAACATTATATCCAATGCTTTAAAACCGGAATATCAAGACAACAT 20 AATGCAACATCTGGTCCGAGCTATCCAGGCAATCACATTTTTGAAGTTCCCCC GGTTATCACACATATATCGATCATACCCCGAAATGTGTAAACACAGATACAGCT CACCATCCCTCTGATAAGATCTTATCAAGTTCGGGCTTGCTCGCTATCGTGAAT TGGGTTGAAGGGTCCGCGATAATTGCATTGGGCATGCCATTGGTAATCACAAT TGGCTGATAATGCTGCTGCTGCAATTCCACGGGTATGAA 25 TTCATCAATTGGTTA	
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003602
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG1347 - novel protein with myosin homology
30	<b>Human homologue of Complete gene candidate</b>	1503990 [dbj BAA13194  (D86958) KIAA0203 similar to mouse CC1.(aa)
35	<b>Putative function</b>	similar to coiled coil protein with ubiquitin like domain
	<b>Confirmation by RNAi</b>	Marked reduction of G1 and G2/M indicating fewer cycling cells
40		



**Example 17 (Category 2)**

	<b>Line ID</b>	703/16
	<b>Category</b>	Meiotic defects in testis: segregation defects, meiotic failure (Mf-07/75)
5	<b>Reversion</b>	R
	<b>Map Position</b>	83B
	<b>Rescue ID</b>	2E7E
	<b>Rescue Sequence</b>	
10	AAGCAGCCCCAACAGCTACGCAAAAAGTTACTTATATTTCGCAGCAAAACAGAT	
	TTTTTTGTTTTAATCGTAAGTATAGGAGTGAAAAATAGCGCTAGAGTAGACCT	
	AAGTACACAGAAAGACAAATAGGGCGAGTAAAATCGCGGTCCTGGTCATTTTC	
	TCTGGCCTTGACCAATCCTTTGTCTGCGCTTTCGTTGGAAAAGGGGTTATGTAC	
	GAACTGCGTGCGTACCTAAGGCCAGATTAGTCATCGGGCAGTCATATATTCAT	
15	GCAAAAAATCATTTGGTGGCCGTCGGCCTTTGTTGACTGTACCTTGCTCATT	
	TTTAATAAGCGCGACAGCAATATACACACTTTGAACCCCCATCCCACATTTTTT	
	CTCACCGTTTCCCCCTAATTTTCGTTTTCCCTGTGCCCATCATTCGCTTTTCGCC	
	ATGTCAGTGTATCGCTTCAAAAATGGCGCCGAACCACATGTCTTCGTTCTCGGC	
	TCGTCCGCTTCGTTTCGTGCGCTCGTGTGTCGTCTCATTCGCTCTCCGAATTCG	
20	TTTAACAAAGTGTTGCGAGCAGAGGGGCCGCTGGATTTCGAGGCAAACAACAC	
	ATATACCTA	
	<b>Genomic hit, Accession No.</b> CSC:AC013960	
25	<b><i>Drosophila</i> EST</b>	several including LD15903 (AA440858), GH20091 (AI389018).
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003602
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG2922 – novel
30	<b>Human homologue of Complete gene candidate</b>	286001 dbj BAA02795  (D13630)
		KIAA0005 [Homo sapiens] also
		NP_054757.1  HSPC028 protein
		[Homo sapiens] e-179
35	<b>Putative function</b>	Weakly similar to a region of human and murine EIF4G2 translation initiation factors; may act as a translation initiation factor
	<b>Confirmation by RNAi</b>	Only wild type profiles observed

**Example 18 (Category 2)**

	<b>Line ID</b>	741/3
	<b>Category</b>	Meiotic defects in testis: segregation defects, meiotic failure (Mf-05/31)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	88D
	<b>Rescue ID</b>	H6E
10	<b>Rescue Sequence</b>	GCCTGGAGCCACCTCTAGAGCCACGGCCAAAAAATTGTGTGCCAAAAAATCG TATGGCGTTACGCATCTTGTTATTCTAGTGTCTTTGGTTCTACAAATCTGGCCA ATGGGATGGACGGATTTTGGGGCTTTTGCGCCCCACATATGTNTCTTACAACC CACTCGGCCCCGGCAAGTGGGTGTCAATTACGGACATCGGCAATCCGAAGACC 15 GGAGACCCAGAGACCCCTCAGACCCCAGGGCCCCATTTCGATTTCGATTTCGAGTT GCGTGGGCCGATCTCACATTAGTCACATCGAAGGAATGAAATAAAAAGAAAA AACATGACGGCCGAAAAGAACTTATCCATCTTCAAAGCTCTCAGAAAATACA AAAAACTAAAAAACTTTTGACTCTTCGTCTTTCACATTTTCGAAATCACAAAAT GTCTGCCATAAATTCCAAAGTGAACAATTGAAATAAATTTTTGCGCCATGAAC 20 ACGCCGACTG
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003705
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG12600 - novel protein
25	<b>Human homologue of Complete gene candidate</b>	CG12600- 5e-27 4240227 dbj BAA74892.1  (AB020676) KIAA0869 protein [Homo sapiens]
30	<b>Putative function</b>	putative cytoskeletal structural protein
	<b>Confirmation by RNAi</b>	Reduction of G1 and G2/M peaks indicating fewer cycling cells

**Example 19 (Category 2)**

	<b>Line ID</b>	773/1
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects, meiotic failure (Mf-02/15)
5	<b>Reversion</b>	R?
	<b>Map Position</b>	83F
	<b>Rescue ID</b>	2D9P
10	<b>Rescue Sequence</b>	CCACCGCCCATGCCGCCATTTATTGAAAGGCCTGTACGCAGTTTGTGTTTTGTTT TTCTCTTTTTTGCTAGCTCAAACACAAAATTACTTTTTGTGGCTTGACTGGTGA GGTCTCTCTATCTCGCTTTTTTCGTCTTTACCTCGCTCTCATTCCTCTCTATCTG CCCTGCTTCCTCTCACTATCTATCTACAACCTGAGGTCAACAAAATAAGTGCGT 15 AGTCAAAAATGTAATTGAATTGATTGACAAACACAGCGAACGTAAATTTCCGT AATGTTTAACCTTGAATTCAAATGAACAACTGTATAAATATAATACACGGGTT AAACTCCATTTCAAAGCAAGCTAAAACATTTTAAATACATTTTAGGGAAACGG CCAATTAAAAGAATAATATTGTGGGGATCAATCTGGGGAAAAATGCAGTATC AGTAATGCTGAATATTTATTTTACTAAATTACAATGAAATGTCTCAAACAAAT 20 GGGTTAATCATTTTCTTGCTCCATCTGCTTTTCCCAACTGTATCCAAGTACAAC TACAGCATTATCCTCAACTG
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003675
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG10272 - novel protein
	<b>Human homologue of Complete gene candidate</b>	CG10272 - 2995577 AC004490 (AC004490) R29381_1(aa) protein includes HMG-I and HMG-Y DNA- 30 binding domain (A+T-hook) found in HMG non-histone components in chromatin
	<b>Putative function</b>	Chromosomal protein
35	<b>Confirmation by RNAi</b>	Loss of G1 peak indicating arrest in G2/M

**CATEGORY 3: METAPHASE ARREST****Example 20 (Category 3)**

5  
**Line ID** 1067/13  
**Category** Mitotic defects in brain: prometaphase arrest  
 (overcondensation, polyploidy, scattered chromosomes with  
 bipolar spindle)  
 10 **Reversion** NR  
**Map Position** 69C4-10  
**Rescue ID** 2F8E  
**Rescue Sequence**  
 15 GTTTGGGCACAGGGTTGTATTTCAATTTATTTTTGGGGGGAGTCGATACGCTCTC  
 TTGGCGTGGTTCGAACGGTCACACTGGCCGAGAGATAACGGAAAATGTTTCAA  
 AGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACTATAATTAGCTTACTA  
 TTCCAAGTATGTATAATTATTACACGTTTAAAAGGCATAACGTTAAGTGTAAC  
 CAAATTATATCAATGGATTTTGAATACCAATATTATTTATTTTATATTTTGAGC  
 20 TTAATATATTAAATCACATATATTTAAGCCTCTTTATATATGTAAATATTTTAA  
 TTTTATTAATAAATTATATATTGTTTTGTAATATGATCGAGGGCTGCCACCT  
 TGTGATAAATGCTTACCAACACTTTTAGGTACGCCGTTTAGTGTACGTAAGTTG  
 CGTACCTAGATATCCAGCGAAATCAAAACATTGAGTAAATCGTGGAATAATGG  
 ATGAAAATAGCTTAATCTACGGACTCGAACTGCAGGCGCGGGCTTTAACACCT  
 25 CAGTACGGAGAGAGCAACGATGTGTGCTTCTTCATAGCCACCAACTCCTTGAA  
 GCCCACCAATCAGGTTCACTTAATCCAGTACGAAGA

**Genomic hit, Accession No.** CSC:AC020333

30 **Associated ORF**  
 Genscan: ORF1 predicted sequences: >16:51:11|GENSCAN\_predicted\_peptide\_2|178\_aa  
 MAQNISPEQSGGAGGGGSKHSDDSM PVKDNHAVSKRLHKELMNLMMANERGIS  
 AFPDGENIFKWVGTIAGPRNTVYSGQTYRLSLDFPNSYPYAAPVVKFLTSCFHPNV  
 DLQGAICLDILKDKWSALYDVRTILLSIQSLLGEPNNESPLNAQAAMMWNDQKEY  
 35 KKYLD AFYEKHKDT

>16:51:11|GENSCAN\_predicted\_CDS\_2|537\_bp  
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 aaagacaatcacgccgtgagcaaaagactgcacaaggaactgatgaacctgatggccaacgagaggcgatctcagcgtt  
 40 tccggacggcgagaacatctcaagtgggtgggcaccatagcgggtccacggaacacgggtgtattcggggcaaacgatcgttt  
 gtactggatttcccaattcctatccgtatgcagcaccgtgggtgaagttcctgacgtcctgcttccatcccaatgttgatctgcagg  
 gcgcacatctgtttggacatactgaaggacaatggcggccctgtacgatgtgcgcaccattctgctgtccatacaatccctgctgg  
 gcgaaccgaacaacgagagtcactgaatgcgcaggccgcgatgatgtggaatgac

- Drosophila* Gene Hit** TBLASTX with ORF1: poor homology to several sequences including homolog of RAD6 (DHR6) (M63792), bendless (L20126 ) and Ubc D1 mRNA for ubiquitin-conjugating enzyme (X62575).
- 5    **Human Homologue** TBLASTX with ORF1: ubiquitin carrier protein E2-C (UBCH10) (NM\_007019.1) and ubiquitin-conjugating enzyme E2B (RAD6 homolog) (NM\_003337.1 ).
- 10    **Annotated *Drosophila* genome genomic segment** AE003541  
**Annotated *Drosophila* genome Complete gene candidate** CG10682 – vihar ubiquitin-conjugating enzyme
- 15    **Human homologue of Complete gene candidate** gi5902146  
0B6F58A1F0665D9A  
|ref|NP\_008950.1| ubiquitin  
carrier protein E2-C [Homo  
sapiens] (2.50E-50)
- 20    **Putative function** Cyclin specific ubiquitin conjugating enzyme
- 25    **Confirmation by RNAi** Complete loss of G1 and G2/M peaks indicating fewer cycling cells. Immunostaining shows metaphase arrest with condensed chromosomes

- Line ID** 1105/1  
**Category** Male sterile, Female sterile, Mitotic defects in brain: prometaphase arrest  
(Overcondensation, polyploidy, fewer anaphases, high mitotic index, scattered chromosomes with bipolar spindle)  
**Reversion** R  
**Map Position** 69C
- Rescue ID** A5B  
**Rescue Sequence**  
GTACATATAATCACAATTGAGAATCGAAAACCCGACCGCCACGAAGCGCGCT  
AAATTACACGCACATACTGAAAGCCAAACAGCGGATAGCACTAGCATCCTAC  
ATATATAGACGTAGATATATAGTCATGGCGCAGAATATCAGCCCCGAGCAAA  
GTGGTGGAGCAGGCGGCGGCGGCAGCAAGCACAGCGATGACTCCATGCCCGT  
GAAAGACAATCACGCCGTGGAGCAAAAGGTGAGTATCATATGGTGCAGCCTA  
AGATAATCCGCCAATATACACACACACTCACACTACCCACAGACTGCACAA  
GGGAACCTGATGAACCTGAATGAATGGGCCACCGAAAAAAGGGG
- Rescue ID** A5E  
**Rescue Sequence 2**  
ATATGTACTGTATAGTGGAAATTTAGTTTGATCGGTCCGAATACGCGTCTGTT  
GCTTTTTTCAGATATTTTTTTTTTCACTTTTGTGTGAAAACAAAATGGAAGGAGA  
ACGAGAAGAACTGTGTTTGGGCACAGGGTTGTATTTCATTTATTTTTGGGGG  
GAGTCGATACGCTCTCTTGGCGTGGTCCGAACGGTCACACTGGCCGAGAGATAA  
CGGAAAATGTTTCAAAGGTAAGTAAAGATTATAAACGTATTAAGCTTAATACT  
ATAATTAGCTTACTATTCCAAGTATGTTATAATTATTACACGTTTTAAAAGGCA  
TAACCGTTAAGTTGTTAACCCTAATTATATCAATGGATTTTGAATACCAATATT  
ATTTATTTTATATTTTGAGCTTAATATATTAATCCACATATATTTAACCCCCCT  
TTATATATGTTAAATATTTTAATTTTATTAATAAATTATATATTGTTTGGTTA  
AAA
- Genomic hit, Accession No.** AC007328 69B-69C
- Associated ORF**  
Genscan: ORF1 predicted sequences  
>/tmp/aaaaanjda|GENSCAN\_predicted\_peptide\_1|357\_aa  
MGKKAKHKKKKGKPEKTAMKADKKQAARQKKMLEKLGEANIADIQLLEAKEG  
KIEAISESVCPPTPRSNFTLVCHPEKEELIMFGGELYTGKTTVYNDLFFYNTKTV  
EWRQLKSPSGPTPRSGHQMVAVASNGGELWFPNFACISRNQSWFVFHNCRLKAA  
SREKVLNFNFTVLPANNIIVHVKLFKKANGFKPWLLDVKLDACRFVRTNFHPF  
VRIIFDLFKDFSTINHTCPYVVLRSRMRYIVRRSPRLVHPIVDVPAIGHTRPRRKA  
RGIGCAHRCPLIRMATPCRTNVMMTMLMRGVSRSRVMAICCYRRPAIAIARRRHP  
TAIAHSQEVAERLGGLLYPDIQRTNP
- >/tmp/aaaaanjda|GENSCAN\_predicted\_CDS\_1|1074\_bp  
atgggcaaaaaggccaaacacaagaagaaggccaaaggcccgagaaaaaggccatgaaagcggacaaaaagcaggcgg  
cgcggaagaaaatgctgaaaaactgggagaagcaaatatagctgatcatccaattgctggaggccaaggaggcgaag  
attgaagccatcagtgaatccgtttgcccgccaccaactccacgatccaattcaccttagtttgccatccggaagaggagctc

atcatgtttggcggcgaactgtacactggcacaaaaaccacagtgtataacgattgttctttacaacacccaaaaccgtcgagtgg  
aggcagctgaaatcgccatcgggaccacgcccagaagtggacaccaaagggtgctgtggcagcaatggaggagaactct  
ggtttccgaacttcgctgtataagtcgcaatcaatcctggtttgtgtccacaattgtcgtctgaaggcggccagtcgtgagaagg  
cttactcaactttaatggaacgggttacatccggccaataacataatgttcacgtcaagctgtttaaaaaggccaacggtttaagc  
5 cttggttattagacgtaaaactcgatgcttgcgtttgtcgggaccaactccatccgtttgtacgcattatattcgatctcttcaagat  
ttctccaccataaaccacacgtgcccataatgtggtcctccgatcgatgcggtatattgtccgcatccccacgacttgtgcacccc  
atcgtagatgttcggctattgggcacactcgcctcgacggaaggccggttcgtggcatagggtgtgtcatcgctgcctct  
gattcggatggcgactccgtgtgtaccaacgtggtgatgatgacgctgatgagggtcggtgagatcgagggtgatggcgatt  
10 tgcgtgctaccgccgaccgccattgccatagcccgtcggcgccacccactgccattgccactcccaagaagttgctgaacgc  
ctcgggtggtcttcttaccggacattcagagaaccaatccgtag

*Drosophila* EST      several ESTs including LD04777 (AA201675)

All other entries as for 1067/13.

**Example 21 (Category 3)**

	<b>Line ID</b>	1407/13
	<b>Category</b>	Mitotic defects in brain: (weak overcondensation, metaphase with bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	92B1-3
	<b>Rescue ID</b>	2D3P
10	<b>Rescue Sequence 1</b>	ATCACGAATTTGACATTGCTACCACATTCGGTGCGTGGACTCTGAAAGCTCTG AGTGTTTTGTTTATGCAAAGCTTTTTTGGACTATCGCGTGGTAAGTAGCCGAAA GAGAAAGCTCTCTTATACGGAAGATGAAGAGTGTGATTCATGAAAATGTATA AGAACGCGGGTCCAAAAAGTCAAGGGAGTTCTAGTGAAATGAAAAGTTCCAA 15 AGGTTTTGAAATCGTTTTATTTCTCGTTCGTATAATTATTGGGTGTCGATCTTT GTTGGGCAGTGTAAGCACAACTTTGAGCTTCATCATACATATCATATGTAA AGCCGGGACGAAAGCTTATGATTCTGTAAAGTGTCCGCCCAAGATAACATTC TCCAGCCCTTCAAATCTTCAAATAAATACGGCTTAAGGCGAGCAAATTTGTAA ATCAAATGATTTGTAAATAAACATTATATGTATTTATCATGCCAGGTTAGAA 20 CACATTGTGCTGATGCAAATAAAATTCCAATTAAACGCCCTGAATGGGAAGA TGACGCATCTTTAATGGGAATATTATGGTAAATTTAATA
	<b>Rescue ID</b>	2D3E
	<b>Rescue Sequence 2</b>	TNCGTGATTATCAGCGTTAATTGTACAATATTATGATTTATTCGAGCTGTAAAT 25 CTTCACAGCAAGCACAACTGTAATTATACCACTTAGAATTCCGCGGAATTAA TTCTTGAAGACGAAAGGGCCTCGTGATACGCCTATTTTTATAGGTAAATGTCAT GATAATAATGGTTTCTTAGACGTCAGGTGGCACTTTTCGGGGAAATGTGCGCG GAACCCCTATTTGTTTATTTTCTAAATACATTCAAATATGTATCCGCTCATGA 30 GACAATAACCTGATAAATGCTTCAATAATATTGAAAAAGGAAGAGTATGAG TATTCAACATTTCCGTGTCGCCCTTATCCCTTTTTTGCGGCATTTCCTTCCT GTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTG GGTGCACGAGTGGGTACATCGAACTGGATCTCAACAG
35	<b><i>Drosophila</i> EST</b>	LD05707 (AA246767)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003727
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG7444 - very short ORF with EF hand homology
40	<b>Human homologue of Complete gene candidate</b>	none
	<b>Putative function</b>	Possible calcium binding protein
45		



**Confirmation by RNAi**      Slight loss of G1 peak

**Example 22 (Category 3)**

	<b>Line ID</b>	1439/7
5	<b>Category</b>	Mitotic defects in brain: prometaphase arrest. (overcondensation, polyploid, no anaphases, scattered chromosomes with bipolar spindles)
	<b>Reversion</b>	?
	<b>Map Position</b>	96F10-14
10	<b>Rescue ID</b>	G3X
	<b>Rescue Sequence</b>	
	GTCGGATGTAGAAGACGTGCCCCGAAACCCAGTTAGAAATCGATGTCAGCGAT	
	GGCGCCGGACTGGAGGATGAGGATGATGACGATATGGAACAGATTACAGCTC	
	AGAAGGTAAGGTAAATCGTAACAGAGCTTTTAAATACGCAAGTAATCACATTC	
15	TGATATCCCTAGGTTCTGGAAATCATAGAAACCGCGTGGATAAATGAAATGTG	
	TGCGCCGGAGATCCTGCCAGCCAGACGGACATGCTGGAGCTGATGGTCTCCC	
	AGGTGGCCCATATGGAGGAGCAGATGCGCGATCTGGACAAGAACGATTTCCG	
	AGCGGTGGTGCACCTCCATGGAACCTGGAGAGGGTGGCTACATAATGGCCAGT	
	TATCTGCGTTGCCGCCTGCAGAAGATCGAAACCTTCACGCAGCACATCCTCAA	
20	CCAGGAGGAGAGCCGTGAGCCGGATGACAAACGTCTGTCTCCCGAGGAGACT	
	AAGTTCGCCCAGGAGTTTGCCAGTAAT	
	<b>Genomic hit, Accession No.</b> AC007825	
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	

AE003754

CG14549 – novel

none

no homologies which indicate function

Only wild type profile observed

**Example 23 (Category 3)**

**Line ID** 1466/4  
**Category** Mitotic defects in brain: metaphase arrest.  
(overcondensation, no polyploidy, fewer anaphases, metaphase  
5 with bipolar spindle)  
**Reversion** NR  
**Map Position** 72F

**Rescue ID** ESE  
10 **Rescue Sequence 1**  
GGCTGGATGCGATTCGCTTTCGGATTTCGGATGGATTTCAGCCGCTGTCTCGACA  
CCGCCGCAACCGCTCTCGGGAGTTTGAAAATTTGAAATGAGCGGATTCGCGTT  
GCGAAGGCGAGCTAGCGTTGCAGGCAGTGTGGCCAGATGCCGCGTGCGAACG  
TATTCTCGAATGCAATCGGCCGAGTGCAGATGCACTAAAAATAACCCACTTCC  
15 AGTGACTGGAAATTAAGATCAAGGNAATAGATTTTATAAAAACTTATATGAGT  
AAAAATTTTAAATTTGTGGAGTCAACCTAAATTATAAGCAACTAATTTATAAC  
ACAAGTAAAGAATGATATTAAGTAACTTTTTAAATAATATTCCATTATGCTTA  
CGCTCAATTTATGAACAAATGTTTTCTCGATCCTTAGGTAAAGTTTCGAGTTTC  
GCGACTANATTTATTAATAAATTAAGAACATCTCCATTTATGTACACATTTAAAG  
20 ATTTATGAGCGGTAATATTAGCTGGTTGAC

**Rescue ID** ESP  
**Rescue Sequence 2**  
ATCCAGCCAAGATATCCTATCGTGCAGCTGAAACCCGAAACCCGAATCCGAGT  
25 TCGAAACGAAACGAATCGCAGTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCT  
CTCTCTCGCGTGTGTGTATGTGTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAA  
TCTTTTCTAGCTGAAAGAAAGCGCAACTTCAATTAGCGAAAAGCAAGAGTAGCT  
AACAAAAAGAAAAGCGGATCGAAAAGTAAAGAAAAACAAAAAACA  
AAAGCAACAAATCGAAATGGCAAGCGAAGTGGCCCAAATACCCGCCGAGGG  
30 AAACGCCCCGAGTGGCGGCGGCGGAAAAATCAGAGGAGCCGGAAAAGTCAG  
CGGCCCCGCCAGCGGACTCAGCGCCGCTCCAGCTGCCGCCCCCGCAGTGGA  
GAAGGCTGAGGATGCCGATGGCGAAAAAAGGACGGCGAGGCCGGAAAGCA  
GGACAAGCAGCAGGATGGC

35 **Genomic hit, Accession No.** CSC:AC020154

**Associated ORF**  
Genscan ORF: ORF2 predicted sequences  
>21:06:03|GENSCAN\_predicted\_peptide\_5|415\_aa  
40 MASEVAQIPAEETPAVAAAEKSEEPEKSAAPPADSAAAPAAAPAVEKAEDADGE  
KKDGEAGKQDKQDGEPPKKDEAVAAPVATKSEAPPAQKFNVHKTNFEKDIIYL  
YQFSRTPLPSLSPYCLKVETWLRVLVGLKYENVDHKMRFRSKKGQLPFIELNGEEI  
ADSAIIKELSSKYEKYLDSGLTAEQRNVSYATIAMLENHLIWIIFYWRAKYPDNV  
LKGYKVNQLHALGLRLPNSILNFFFKITFGRKGTKKLKAHGIGVHSAEEIEEFGKD  
45 DLKVLSEMLDCKPFFFGDEPTTLDVVAFAVLSQLHYLSKDIA YPLRDYMTKECPN  
LIGHVSRMKDKCFPDWDEICTKLDLNAHIPKPEPETKEGKEGGEQKSNEQEGTE

GDKIEKELEKDKSNEKESTEENKEKEETK

>21:06:03|GENSCAN\_predicted\_CDS\_5|1248\_bp

atggcaagcgaagtggcccaatacccgccgaggaaacgcccgagtgccggcgccgggaaaaatcagaggagccggaaaa  
 5 gtcagcgggccccgccagcgggactcagcggccgctccagctgccgccccgcagtgaggagaaggctgaggatgccgatggcga  
 gaagaaggacggcgaggccggaaagcaggacaagcagcaggatggcgaggagcccaaaaggacgaggcggtggcagc  
 acccgtggcgaccaaactcggaagccccgcccgccagaaattcaatgtgcacaagaccaacttcgagaaggacatcatctatct  
 gtaccagttctcgcgacccccactgctgccctccctgtcgcctactgcctgaaggtggagacctgctcgtctgtggcctga  
 aatacagagaatgtgatcataagatgctgtcccaagaagggtcagctgccgttcacgagctgaatgggaggaaatcgc  
 10 cgattcgcccatcatcatcaaggaaactgctgtccaaatacagagaagtacctggactcgggactcaccgccgagcaaatgtgctcaa  
 ctctacgccacgattgcatgctggagaacctctcatctggatcatcttctactggcgcccaagtatccggacaatgtgctcaa  
 gggctacaaggtaacttcagcacgccctcggcctgcggctgcccaactcgattctgaacttctttaaagatcacctttggtcgc  
 aagggcacgaagaagtgaaggcgacggcatcggtgtccacagcggcgaggagatcaggagttcggaaggacgacctg  
 aaggtgctcagcgagatgctcactgcaagccttcttctcggcgacgagcccaccacctggatgtggtggccttcgctgtcct  
 15 ctccagctccactatctgtccaaggacattgctatccgtcgcgactacatgaccgagaagtgcaccaacttgattggccacg  
 tatctcgcatgaaggacaagtgttccccgactgggacgagatctgcacgaagctggacctcaatgcgcacattcccaagccag  
 agcccgagaccaaggagggaaggagggtggcgagcaggagaatcaaacgaacaggagggcactgaggggcgacaagat  
 cgagaaggagttggagaaggacaagtcaaacgagaaggagtcgaccgaggagaacaaagagaaggaggaacaaagtaa

- 20 ***Drosophila* Gene Hit** rescue sequence and TBLASTN with ORF2: failed axon  
 connections (U21685)  
**Human Homologue** BLASTX with fax: Metaxin 1 and 2 (Q13505 and AF053551)  
***Drosophila* EST** several including LD31362 (AA951078 similar by BLASTN to  
 U21685 failed axon connections)

25 **Annotated *Drosophila* genome genomic segment** AE003527

**Annotated *Drosophila* genome Complete gene candidate** CG4609 – fax failed axon  
 connectionsconnections

30 **Human homologue of Complete gene candidate** 4505281  
 ref|NP\_002446.1|pMTX|  
 metaxin>gi|3024205|sp|Q135  
 05|MTXN\_HUMAN  
 METAXIN (4e-06)

35 **Putative function** *Drosophila* fax is a dominant genetic enhancer of the Abl mutant,  
 developmentally expressed in axons of the CNS

40 **Confirmation by RNAi** Weak reduction of G1 and G2/M peaks indicating fewer  
 cycling cells

45

**Line ID** 262/20  
**Category** Mitotic defects in brain: metaphase arrest.  
(overcondensation, polyploidy, aneuploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle)

5 **Reversion** NR  
**Map Position** 72F

**Rescue ID** G6E  
**Rescue Sequence**

10 AGCTGCACGATAGGATATCTTGGCTGGATGCGATTCGCTTTCGGATTCGGATG  
GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA  
ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTAGCGTTGCAGGCAGT  
GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA  
GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT

15 AGATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCT  
AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT  
TTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG  
ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAATAAAGAACAA  
TCTCCATTTATGTTCCC

20 **Drosophila EST** several including LD28084 (AA949260)

All other results as for line 1466/4

25

	<b>Line ID</b>	262/22
	<b>Category</b>	Mitotic defects in brain: metaphase arrest. (overcondensation, polyploidy, few anaphases, high mitotic index, metaphase with bent bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	72F
	<b>Rescue ID</b>	F1E
	<b>Rescue Sequence 1</b>	
10		AGCTGCACGATAGGATATCTTGGCTGGATGCGATTTCGCTTTCGGATTTCGGATG GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA ATTTGAAATGAGCGGATTTCGCGTTGCGAAGGCNAGCTAGCGTTGCAGGCAGT GTGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCA GATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAAT
15		AGATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCT AAATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTT TTTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCG ATCCTTAGGTAAAGTTTCGAGTTTCGCGACTAGATTTATTAAAATTAAGAACA TCTCCATTTATG
20	<b>Rescue ID</b>	F1P
	<b>Rescue Sequence 2</b>	
		GTGCAGCTGAAACCCGAAACCCGAATCCGAGTTCGAAACGAAACGAATCGCA GTGGTGGTTTCTCTCTCGCTCTCTAGCTCTCCCTCTCTCTCGCGTGTGTGTATGT
25		GTGCGAGTGGCAGGAAAAGTGCGAAGCCGAAATCTTTTATAGCTGAAAGAAAG CGCAACTTCAATTAGCGAAAAGCAAGAGTAGCTAACAAAAAGAAAAGCGGAT CGAAAAGTAGAGAAAAACGAAAAAAAAAAAAACCAAAGCAACAAATCGAAATG GCAAGCGAAGTGGCCCAAATACCCGCCGATGAAACGCCCGCAGTGGCGGCGG CGGGAAAAATCAGAAGAGCCGAAAATCAGCGGGCCCGCCAGCGGGACTCTG
30		CGGGCGCTCCAGCTGCCGCCCCCGCAGTGGAGAAGGCTGAGGATGCCGATGG CGAA
	<b>Drosophila EST</b>	several including LD28084 (AA949260), LD38479 (AI518768)
35	Other results as for line 1466/4	

	<b>Line ID</b>	262/3
	<b>Category</b>	Mitotic defects in brain: Metaphase arrest (overcondensation, polyploidy, aneuploidy, no anaphases, high mitotic index, metaphase with bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	72F
	<b>Rescue ID</b>	H3E
	<b>Rescue Sequence</b>	
10		AGCTGCACGATAGGATATCTTGGCTGGATGCGATTTCGCTTTCGGATTTCGGATG GATTCAGGAGCCGCTGTCTCGACACCGCCGCAACCGCTCTCGGGAGTTTGAAA ATTTGAAATGAGCGGATTCGCGTTGCGAAGGCGAGCTATCGTTGCAGGCAGTG TGGCCAGATGCCGCGTGCGAACGTATTCTCGAATGCAATCGGCCGAGTGCAG ATGCACTAAAAATAACCCACTTCCAGTGACTGGAAATTAAGATCAAGGAATA
15		GATTTTATAAAAACTTATATGAGTAAAAATTTTAAAATTGTGGAGTCAACCTA AATTATAAGCAACTAATTTATAACACAAGTAAAGAATGATATTAAGTAACTTT TTAAATAATATTCCATTATGCTTACGCTCAATTTATGAACAAATGTTTTCTCGA TCCTTAGGTTAAGTTTCGAGTTTCGCGACTAGATTTATTAATAAATTAAGAACATC TCCCTTTATGTTC
20		Other results as for line 1466/4

**Example 24 (Category 3)**

	<b>Line ID</b>	238/20
	<b>Category</b>	Mitotic defects in brain: metaphase arrest
5		(overcondensation, metaphase with bipolar spindle)
	<b>Reversion</b>	NR
	<b>Map Position</b>	75E1-3
	<b>Rescue ID</b>	D7E
10	<b>Rescue Sequence</b>	TTCAGTCGCGCATTTACCGTTTCCGAATCGGACGAACCGGGCGTGATTGCTC TCCTGCTGCTTTCGAGATCGGAGTCCCGATAAGGATATAACTACAACCTAAAG AGGAATCCAAGCCTCCTCCTGCCGCTAGTTTCGAAAAGTAAATAGAGTACTTG TTATCAACTGGGGAAGCGGAGATACATAGCTCCGATATTCCTGTGAAAGCCAG 15 ACAAACGGATACCAACGAACAATCGCCATGTGCGTCGTCGTCCTTCTCGTTT CACACATCGTGCGATAAAAATACCGCTTTGCTTTTTGTGTTTATTTAAAAATTT TGGTTAGGAAGTGAACCTCGAAGTCTGACGTTTGCATTTTCAACAACAAAA AGAGCAAAACATAGCAGAAGAACCCAGAAAGAAACAGGAACAGAAACCGTT GACCGAGTGCCAGTGTGAAGGTCTAGGCACAAAGAACGCTACCAAGAACTCT 20 TGGGAGTTAGGGAGGCTCTTTACAATGACAACATTGCACCAAAGATGGACTCT CTCTCTAAAATGCATTTTCATACCAATATTTACTTT
	<i>Drosophila</i> EST several including LP04802 (AI260815)	
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003519
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG3979 - novel gene with homology to sodium- dependent dicarboxylate transporters
30	<b>Human homologue of Complete gene candidate</b>	3e-87 4506979 ref NP_003975.1 pSLC13A2  UNKNOWN >gi 2499523 sp Q13183 NDC1 35 _HUMAN RENAL SODIUM/DICARBOXY
40	<b>Putative function</b>	sodium/dicarboxylate transporter
	<b>Confirmation by RNAi</b>	Only WT profiles observed



**Line ID** 490/9  
**Category** Meiotic defects in testis: segregation defects, multipolar spindles (Mul-02/29)  
**Reversion** NR  
5 **Map Position** 95C1-8

**Rescue ID** I4E

**Rescue Sequence**

10 GCTCTGCCGCTTCAACCGCCCGCCTTCTGTGTGTTGGTGTGCCGCGACGTAGG  
GCTAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGAGAGCGGGAGAAGA  
GCAGAACGTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT  
AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA  
TTATTGAAATCATTATTTGATGGTCTATGGGGGTTTCTTTCGTAGTTATTCAT  
AGATCGGCGATTAAAGCTACGCTTAAAGGGTAATTTGTCTGAGATATCTTTGT  
15 CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG  
CCAGCTTTTCAGCAGAGTTCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA  
ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA  
CCATTTGTACGTTTTTAAATTAAAGTATTTTGATTTTCACTAATACAGGCTCTAA  
GCTGATCCAAATCTACAAGCTTAGTTTTTGAATAGTCTTCACATGTTGACTTTT  
20 ATTCTCT

**Genomic hit, Accession No.** CSC:AC015160

*Other results same as 238/20*

25

	<b>Line ID</b>	660/3
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects, abnormal spindles. (Ab-01/03)
	<b>Reversion</b>	R?
5	<b>Map Position</b>	75E
	<b>Rescue ID</b>	H8E
	<b>Rescue Sequence</b>	
10		GCTCTGCCGCTTCAACCGCCCGCGTTCTGTGTGTTGGTGTGCCGCGACGTAGG TGTAGGGTCCGCTGCACACGTGTGTGTGGGAGCGCGAGAGCGGGAGAAGA GCAGAACGTTTTTTGGGCGGCTAGTGGTGGCACCGTGAGCATGCCGGTCGTCGT AAGATAGGCTTAGGAACACTCAGAGAAAATTTGTTTAGCTCAGCATTTTCCTA TTATTGAAATCATTTATTTGATGGTCTATGGGGGTTTCTTTCGTAGTTATTCAT AGATCGGCGATTTAAGCTACGCTTAAAGGGTAATTTGTCTGAAATATCTTTGT 15 CATTTAAAGTTAAGTCTCAGCTTATCCAAAAGTCAGTTATTGGAAAAAAGGAG CCAGCTTTTCAGCAGAGTTCCGGCTTAAGCGCTTATTATCATATTAACCAGCTTA ATTAATGTATCTTTTAAATTGTTATATGCATTAAATCACTAATTAAGGTGATTA CCATTTGTTTCGTTTTTAAATTAAAGTATTTGAATTTC
20	<b>Genomic hit, Accession No.</b>	CSC:AC015160

Other results same as 238/20

**Example 25 (Category 3)**

	<b>Line ID</b>	273/18
5	<b>Category</b>	Mitotic defects in brain: metaphase arrest (overcondensation, very high mitotic index, few polyploids, metaphase with bipolar spindle )
	<b>Reversion</b>	NR
	<b>Map Position</b>	75E
10	<b>Rescue ID</b>	D1E
	<b>Rescue Sequence</b>	AACTGGGCTAAAACCAGCTGAAAAGTGGTAAAAAGTAAAATATTTGGAGAAG GAAAGCCTTAAGTTCCTCTCTACGCTTCGTACACGTAATGTGCGTGGTTAATC TACGTAAACAAGTGGAAACCATGTTACGTGCCGTGGCTTTGTGTGTGTCAG 15 TGGTGCTCATAGCACTATATACGCCAACTTCTGGGGAATCCAGTCAGAGCTAT CCCATACCACGCTAATCAACGCGAAATGGACGCAGACGCCCTATATCTGGA AATCGCCGAGTATCTGGCCGATGAGCAGCGGGCCTCTTCTGGGATTACGTTT CGGGGGTGACAAAGTTGGACACGGTTCTCAACGAATATGGTTTGTGTTTATAA GTCATGGAGAACCCGCATTAAAGAGCTTTTTATATTCTCCTCAATGTGAATCC 20 GAATCCATATAAAATC
	<b>Genomic hit, Accession No.</b>	AC015160
	<b>Associated ORF</b>	
	Genscan: >ORF2 predicted sequences	
25	>16:57:34 GENSCAN_predicted_peptide_5 1548_aa	MLRAVALCVSVVLIALYTPTSGESSQSYPTTLINAKWTQTPLYLEIAEYLADEQA GLFWDYVSGVTKLDTVLNEYDTESQQYNAALELVKSHVSSPQLPLLRLVSMHS LTPRIQTHFQLAEELRSSGSCQSFTFAQVGSELACSFNELQKKLEVPLAKDSLDA VVTYSFDHIFPGSENNTRTVVLYGDLGSSQFRTYHKLLEKEANAGRIRYILRHQLA 30 KKDKRPVRLSGYGVELHLKSTEYKSQDDAPKPEAGSTSDEDLANESDVQGFDFK VLKQKHPTLKRALDQLRQRLQGNDEIAQLKAWFQDLGLQAAAAIAEIQGDET LQILQYTAHNFPMRLARTLLAHKVTDGLRAEVKHNTAFGRSLNVAPPDGFALFING LFFDADTMDLYSLIETLRSEMRVLESLSHNNVRGSLASSLLALDLTASSKKEFAIDI RDTAVQWVNDIENDVQYRRWPSSVMDLLRPTFPGLRNIRKNVFNLVVVDAL 35 QPTARSVIKLSESVIHQAPIRLGLVFDARDANEDNLADYVAITCAYNYVSQKKD ARAALSFLTDIYAAVGETKVVTKKDIVKQLTKEFTSLSFAKAEFLEEDSTYDYGR ELAAEFIQRLGFGDKGQPQALLNGVPMPSNVVTADSDFEAAIFTEIMTHTSNLQKA VYKGELTDNDVAIDYLMNQPHVMPRLNQRILSQEDVKYLDINGVAYKNLGNVG VLNRLSNRDMTATLMDNLKYFGGKKSTELIGRASLQFLTIWVFADLETQGRDLL 40 THALDYVQSGESVRVAFIPNTESSASSRRNLNRLVWAAMQSLPPTQATEQVLK WLKKPKIEIPTQLEDILGSTELHLKMLRVYSQRVLGLNKSQRLVIGNGRLYGPL SSDESFDADFALLARFSSQYSDKVRQVLKESAQDVNEEFNSDTLLKLYASLLPR QTKTRFKLPTDLKTDHSVVKLPPKQENLPHFDVAAVLDPASRAAQKLTPILILLRQ VLNCQLNLYLIPVPQHSDMPVKNFYRYVVEPEVQFEANGGRSDGPLAKFSGLPAN 45 PLLTQQLQVPENWLVEAVRAVYDLNKLTDIGGPVHSEFDLEYLLEGHCFDAA SGAPPRGLQLVLGTQSQPTLVDTIVMANLGYFQLKANPGAWSLRLREGKSADIYA

- ISHIEGTNTHHSAGSSEVQVLITSLRSHVVKLRVSKKPGMQQAELLSDDNEQAAQS  
GMWNSIASSFGGGSANQAATDEDTEINIFSVASGHL YERLLRIMMVSLKHTKSP  
VKFWFLKNYLS PQFTDFLPHMASEYNFQYELVQYKWPRWLHQQTEKQRTIWGY  
KILFLDVLFP LNVRKIIFVDADAIVRTDIKELYDMDLGGAPYAYTPFCDSRKEMEG  
5 FRFWKQGYWRSHLMGRRYHISALYVVDLKRFRKIAAGDRLRGQYQALSQDPNS  
LSNLDQDLPNNMIHQVAIKSLPDDWLWCQTWCSDSNFKTAKVIDLCNNPQTKEA  
KLTAARIVPEWKDYDAELKTLMSRIEDHENSISRDSA VDDSVDDSVETTVTPS  
HEPKHGEL
- 10 >16:57:34|GENSCAN\_predicted\_CDS\_5|4647\_bpatgttacgtgccgtggcttgtgtgtctgtgtgtctca  
tagcactatatacgcacacttctggggaatccagtcagagctatcccacacgtaatacgcgaatggacgcagacgcc  
cctatacttgaaatcgccgagtagctggccgatgagcaggcggccctctctgggattacgtttcgggggtgaccaagtgggaca  
cggttctcaacgaatatgataccgagtcgcaacagtacaatgccgccttgagctggtcaagagccatgtgagttctcccaattg  
cccctgcttaggtggtggtatccatgcatagcttgacgccccggatccagaccacttcagttggccgaggaaactgaggagca  
15 gtggctctgtcagagctttacttttggccaggtgggttcggaactggcctgcagcttaacgagctgcagaagaagctggagtg  
cgctcgcaaggtagcttgatgcttctgtgtcacctacagcttgatcacatttccctggcagtgagaacaatacccgactgt  
ggtactatagcggcatttgggaagctcgaatccgcacatcacaaaactattggaaaaggaaagccaatgctggccgattcgtta  
catcttgcgtcatcaattggcaagaaggacaagcgaccggtacgacttgggctatggagtggaactccatctgaagtaacg  
gaatacaagagtcaggatgatgctcgaagcccgaagctggttccacttctgatgaggatttggctaataatcggacgtccagg  
20 gctttgattcaaggtgctgaagcagaagcatctacactaagagagcgctggatcaactgcgtcagaggcttctcagggaac  
gatgagatcgccaattgaaagcatgggagttccaggatttgggtctccaggcggccgctgtattgcagaatacagggtgatg  
aaacctacaaattctcaatatactgccataatttcccatgttggccagaacctgtgcccacaagggttagcgatggttaag  
ggcggagggtaaagcataatacgaagcatttgaagaagctgaatgtagcgctccagatgggtccctttcatcaatggactctt  
cttcgatgctgacacaatggatctgtattccctgattgagacgctgcgctcgagatgctgttctcgagagctgcacagtaataat  
25 gtgagggtgaagccttgcagctcctgtctgccttggatctgacggcctccagcaaaaaagaattcgccatcgacatccgtgaca  
ctgcagtagcagtggtgaacgatattgaaaacgatgtgcagtagccaggtggccctcatcggtgatggatctttgctccaacct  
ttctggcatgttaaggaatatccgaagaatgtgtcaatttggctctagtgtgtagcgcgtgcagcccacagctagaagtgttat  
taaactgtcagagtcgtttgtcatccatcaagctccattcgttgggttgggtttgatgcgaggagcgaacgaggataatcttg  
cagattacgtagccatcagctgcgcctataactatgtgagtcagaaaaaggatgcccgagctgttaagtttctcaccgacatct  
30 acgcagcagttggtgagacaaaagtgtcacgaaaaagacatagtaagcaactaacgaaggaattacatcattaagcttgc  
caagcggaggagttcctggaggaaagattccagctacgactatggcaggagctgcagcagagttcattcagcggtgggatt  
cggagacaagggacaacctcaggccttgtgaatggtgttccaatgccagcaacgtgtgaccgccgatagcgacttcaggga  
ggctatttccaggagattatgaccacaccagcaatctccaaaaggctgtgtacaaagtgaaactgacagacaacgatgtagcca  
ttgattatctgatgaatcaacctcagctgatgccagattgaatcagcgaatcctaagccaggagatgtgaaatatcttgatattaac  
35 ggctgtgacctacaaaaatcttggcaatgttgagtttaaatcgtctgtctaaccgggatatgaccgtacgctaattgataatcttaa  
atacttgggtgcaagaagtctacggagcttattggccgagcatccctacagttcctaacgatttgggtgttctgatttggaaactg  
accagggtcgagatctgtcaccatgccctggactatgtccaaagtgagagagtggtgcgagtcgattcattccaaactga  
aagctcttccgctcaagccggaggaaatctaactgattgttgggtgccatgcagagcttccaccaactcaagccacggagc  
aggttctcaagtggctaaagaaccaaaggagaaaattgagataccactcagctcaggatatacctgggatctacagagctgca  
40 cctgaagatgttgagagtttattccagcgagtggttgggtctaaataaatccagcgttgggtcatcggtaatggcggtttatggg  
ccccttctgcggatgaaagctttagatagcgccgatttgcgttggtagccaggttcagttctctacagtatagcgataaggtgcgtca  
ggctctgaaggaatctgtcaagatgtcaatgaggaaatcaacagcgatacttgcctaagttgtatgccagcctgcttccaggga  
aaccaaaactcgctttaaagctaccaacggacttaaaaaccgatcactcgggtgtaaaactaccgcccacagagaaatctcccc  
attttagtggccggttggatcccgcctcccgagcagctcaaaaactaacgcaatacttatttgcctcgtcaagtgtgaact  
45 gccaatgaactatcctgattcccgctccccagcagcgatagcccgtaagaactctacagatacgttggaaacggag  
gtccaattcaggcgaatggaggccgatctgatggtccttggccaaattcagtggttggcagccaatcctctgctgaccagca  
gctgcaggttcccgaagactgttggctgaagctgtgagagcagtttacgatctggacaacattaagttgaccgatattgtggac  
ctgtgcacagcgaattcagctggagtagctgttggagggtcactgctttagctgctagcggcgctccgccagaggacttc

agttggtgttgggtaccagagtgcaacctaccttggtagatactattgtgatggcgaatttgggtatttccaacttaagccaatcca  
ggagcttgggtccctacgcttgcgtgaaggcaaatcggcggatattatgcaatcagccacattgaaggaacaatacccatcattc  
ggctggctcttctgaagttcaggttctataacctcttgcgatcccatgtgtgcaaatgaagggtgtctaagaagccagggcatgcag  
caggcggaaactcctgtcagatgacaacgaacaggcagcgcaatcaggcatgtggaacagcatcgccagcagtttggcgccgg  
5 cagtgccaaaccaagcagccactgatgaggatagcgaaccatcaacatttctctgtggcatcgggacactgtacgaacgtcttct  
aaggatcatgatgtttcgtctgaagaacacacaaaatcacctgtgaagttctgttcttgaagaactatcttccgccaatttacgg  
atttcttctcatcatggccagtgtgtagaacttccagtagcaattggctccagtagcaaatggccccgctggctgcatcagcaaacgg  
aaaaacagaggaccatttgggggtacaagatccttttctggacgtgctcttcccgctgaatgtgaggaaaatcatttctgtgtagtgc  
cgatgccatcgtgaagaacggatataaaggagttgtatgacatggaccctcgaggagcaccctatgcctacacgccatttctgcgatt  
10 cccgcaaagagatggaggggcttccgatttctggaagcagggatactggcgaagccatctgatgggcaggcggtaccacatttccg  
ccttgtacgtgtgtgactgaagagattccgcaagattgcggcaggagataggctaagaggccaataccaggcacttagccagg  
atccgaacagcttatccaatttggatcaggacttgcccaacaacatgatccaccaggctgccatcaaatccctgcccagcacttg  
ctatgtgtccaaacgtgtgtgcagcgacagcaacttcaagactgctaaagtattgtgtgaacaacccgcagaccaaggagg  
ccaaactcacggccgcccagaggattgtcccgaatggaaggactacgatccgagctgaagacctgatgtctcgcacatcag  
15 gatcatgagaattcgatagcagggactcggcagttgatgttcggtgacgattcgggtggaggtcaccactgtgacgccttctcat  
gagcccaagcacggcgcagctgtga

	<b><i>Drosophila</i> Gene Hit</b>	rescue sequence and BLASTX with EST and TBLASTN with ORF2: UDP-glucose:glycoprotein glucosyltransferase (U20554)
20	<b>Human Homologue</b>	BLASTX with UDP-GGT: hypothetical protein (AL133051)
	<b><i>Drosophila</i> EST</b>	several including GH16576 (AI293351)

25 Annotated *Drosophila* genome Complete gene candidate ugtUDP-glucose-glycoprotein  
glucosyltransferase

30	Human homologue of Complete gene candidate	CG6850- IGI_M1_ctg14521_41 D65BCE6EEC187AE3 TRANS:SEPT20T.ctg14521.2 2 FPC_ctg:ctg14521 FPC_start:1284609 FPC_end:1284696 FPC_strand:+ (1.20E-215)
35		

**Putative function** ugtUDP-glucose-glycoprotein glucosyltransferase

40 **Confirmation by RNAi** Only wild type profiles observed

**Example 26 (Category 3)**

	<b>Line ID</b>	430/5
	<b>Category</b>	Mitotic defects in brain: metaphase arrest (overcondensation, polyploidy, metaphase with bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	98B5-8
	<b>Rescue ID</b>	2C2E
10	<b>Rescue Sequence</b>	GTGCGGCCCATGGATGTGCGAACGTGTACGAAGACCAAGATCGGCATCGCCA TCGGCGGCAGCACGACGGACGATAACGAAAAAGCTACAGCCGCCGCCACAGA TACAGATGCAGATGCCATGCCGCTGTTATCAGCGCGAGCGGGAGAATGATAA GGGATGGGATCGCTCAGCGCGGCAGGCAAGACGACCAAAAAGAGAGCCAAC 15 TAAATGATGTGCCTAAGACTAAGAGTTTAAATGAGCATTACTGTGCGCACTCT ATGTATTATGAATAAAATTCATACAACTTTGTGGTTTATTATAATATAAAAGT GTGTCAGCTCTACTCGGGGAAAGTAAGTTTACTTCTTGGCCGCTGGCTTCTTG GCGGCGACCTTCTTCTTGCGGGCGGCCAGCAACTTGGCGCGATTGGCGCAGCC TTGGTGGCCACATTGGCGAAGTGCAGCTTGGCCAGCTCGACGTTCTGCTTCTT 20 GGCTTGGCCAGCACCTTGGCCACGGTGCCTTCTCGGCGGCGAGGGCGGCAC GACGCTTGAGTACCTCGGCATAAGGGTTCAACTTGATCAACTTGCGCACGGTT GGTAAGGGGGTT
25	<b><i>Drosophila</i> EST</b>	several including LD45359 (AI513164)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003763
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG5502 RpL1 - Ribosomal protein L1
30	<b>Human homologue of Complete gene candidate</b>	1e-126 432359 dbj BAA04887  (D23660) ribosomal protein [Homo sapiens]
35	<b>Putative function</b>	structural protein of ribosome involved in protein biosynthesis
40	<b>Confirmation by RNAi</b>	Marked decrease in G1 and G2/M indicating fewer cycling cells

**Example 27 (Category 3)**

	<b>Line ID</b>	472/12
	<b>Category</b>	Mitotic defects in brain: metaphase arrest. Meiotic defects in testis: segregation defects. Abnormal spindles (mitotic: High mitotic index, meiotic: Ab-08/24)
5	<b>Reversion</b>	R?
	<b>Map Position</b>	96C7-9
	<b>Rescue ID</b>	2B6E
10	<b>Rescue Sequence 1</b>	GTCTGACGTTCTCTGAGGGCAAAAGTTTCGAGTTAGTTGAAGGTGAGGGTGCT CGATCACCGATTTGCGGTGAGACGAAAGAAAAGTATGCATTGTTGCGTTGTAA AGAGAGCCGCGCTCGTCTTGTTACATTGTCGCTGAGAACGTATGTTGTGCT TCATCATTTTCCTTGTTGATTTCCCTTTGACGTGGCAACTTGACCATGTATGACA 15 ACTCTTTGGTGGTGCCATCTGGAAGGCAGAAATTTGATGTCAACGGTGCTCCC AGCCAGTCCACTCCCCAACTCACCTGCAGCTCCACTTCGATATTAACTCGCA ACATATTAGTGGCGTAGTTGTACCTGCCGCGGATCCCATTTCCGCTTTGAAAT TTCGCACTTTCGAATATCCGTCCACATTCGATTTGAGAACATCTTCGAAACGTT CAGCGGTGACCCAATCGGGTATTTTGCCAGCCGCCATTGTAGATAATCGGGAT 20 AAGTATTTTGAAATCGAGCAGAAAACACATATACGTCCAGTGTGACGGTCTTG CGTAGACTGATGAAAGCCGAGTATTAGACTCTACACATCTGTGGAGCTTTTAA ATTCGTAGTGC GCGGCCGATTCTCTCGATCTTCTCTCAAAAGCTCCGCTAAT
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003751
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG10618 - novel
	<b>Human homologue of Complete gene candidate</b>	none
	<b>Putative function</b>	no homologies which indicate function
30	<b>Confirmation by RNAi</b>	Only wild type profiles observed

**Example 28 (Category 3)**

	<b>Line ID</b>	571/15
	<b>Category</b>	Mitotic defects in brain: metaphase arrest (overcondensation, few anaphases, some polyploids)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	93D
	<b>Rescue ID</b>	2A8E
10	<b>Rescue Sequence</b>	GGCGGCGCTACATTTGTTGTTGTCGCTGCTGCTCACAGCTCCACCACCATTTCG ACAGTTATATTACCTCGCTCAAGTCGCCCTCTCCCTCTCGCCCACTCGCTGTG TCAATCGAATTAACGAATGCTCTTCGGCGAATAATTGGGTTTAGATACTTT TCCAGCAGACAAAGTTGTATTTTTGCACTTCTTATTGATATTAGGCAAAACGC 15 ATCGGCCGAATCACACGCACACAAAGCACACACGCGAGCAGCGGTTTTTCAA TCTGCAGTACACCAAACAACACACACTATTTCCCTAATGCCTGTTCTTATCCCTC TGATATTCCCAATGAATCGCTGGGCAATTGGCGATTCTGAACCGATTTTCACTT GGCTCTTTGTTTTATTTAATTTTCACCGAAACGCTCTCACACGCAGAGACGCTT TTGCTCGTTTCGCTGATGCTTCTGCTGCAATACACACCACCTACGAAACGAGCC 20 AAGGGAAATTGTATCTATGGGCTGTGTATCTGTTTCTACGCGGCACGCGCTGC ACGTCCGCTCGCTTCGGGTTTTCGAGAGAGAATATACTTTTTCGATACGGTA CGGTAAACGAATTCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATA CGCTATTTTATAGGGTAATGCATGATAATAATGGGTTCTTAGACGTCA
25	<b>Drosophila EST</b>	LP07504 (AI294185), LP06548 (AI293427)
	<b>Annotated Drosophila genome genomic segment</b>	AE003734
30	<b>Annotated Drosophila genome Complete gene candidate</b>	CG15802 – novel homology to Doom, a product of the Drosophila mod(mdg4) gene, induces apoptosis and binds to baculovirus inhibitor-of- apoptosis proteins
35	<b>Human homologue of Complete gene candidate</b>	none
	<b>Putative function</b>	inducer of apoptosis
	<b>Confirmation by RNAi</b>	Only wild type profiles observed



**Example 29 (Category 3)**

	<b>Line ID</b>	736/15
	<b>Category</b>	Mitotic defects in brain: prometaphase arrest (overcondensation, fewer anaphases, metaphase with bipolar
5	spindle)	
	<b>Reversion</b>	NR
	<b>Map Position</b>	73C
	<b>Rescue ID</b>	H5E
10	<b>Rescue Sequence</b>	
		CTAATGAGTAAGGAAAACCAATCAGCCTTGCTAATCGCTTGGCAGTATTGGCT
		TCTATGCAGGGGGGCGTGTCCCGCGCCCCCTTGAAGCTCAAATTTTGAAGGG
		CACAGGTCGTCCCCTCCTCCTCCGCGTGGGTGGCGTTCGGCCGAACGAACCGG
		CGCCTACTTTGCGTCCGGCTAGCGAGGATCTCTGGGTGCCACCCACGGCTGG
15		GTGTTGCGATCTGCCCGATTGATAATCCATGCGTGAGAAAGCTTTAGAGAATC
		TGCCAGATTATTACTCCCCGCATACTCAGAAAAATGTATCCTTCAGATATG
		TTTATGTTTATGAAGTGAAAAAAGTCCTTTGAAATACTACAAAAAGTGAGGAT
		CTGACCAATGATTGATTCTATAGAAATATACTATAAACTATAAACTAC
20	<b>Genomic hit, Accession No.</b>	CSC:AC014181
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003526
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG3971 baldspot - with
25		homology to membrane
		glycoprotein
	<b>Human homologue of Complete gene candidate</b>	CG3791-9e-08
		4680391emb CAB41293.1
		(AL034374) dJ483K16.1
30		(novel protein) [Homo
		sapiens]
	<b>Putative function</b>	membrane protein, function unknown
35	<b>Confirmation by RNAi</b>	Slight reduction of G1 and G2/M peaks indicating fewer
		cycling cells

**Example 30 (Category 3)**

	<b>Line ID</b>	82/24
5	<b>Category</b>	Mitotic defects in brain: metaphase arrest (condensation, no polyploidy, no anaphases, metaphase with bipolar spindle)
	<b>Reversion</b>	NR
	<b>Map Position</b>	100D
10	<b>Rescue ID</b>	2E3E
	<b>Rescue Sequence</b>	GGTCAAGCCCGATGGCGTCCAGCGCGGGCTCGTCGGCAAGATCATCGAGCGC TTCGAGCAGAAGGGCTTCAAGCTGGTCGCCCTGAAGTTCACCTGGGTAAAGCGG ATAATTGAATTAGGAAGAAATCAATAGATATACATACGTGGAAACGGGTTC- 15 CCCACGCGGGGTTGCTATCGGACCTAACCTCAAAGGCTGGGTGCAGGCGTCAT CGCGGAATGACATGTGTTAGAGGTCAGAACTGCAATTAAGTATAACGAACC GTTTTGTAACCAGGCCTCCAAGGAGCTGCTGGAGAAGCACTACGCTGATCTGT CCGCCCCGCCCTTCTTCCCCGACTCGTGAAGTACATGAAGTCCGGCCCCGTG GTGCCCATGGTGTGGGAGGGTCTGAATGTGGTCAAGACCGGTCGCCAGATGCT 20 CGGCGCCACCAACCCCGCGACTCGCTGCCCCGCCACCATCCGCGGTGACTTCT GCATTACGGTCGGACGCAACATCATCCACGGCTCCGATGCCGTCGAGTCTGCC GAGAAGGAGATCGCCTGTGGTTCAACGAAAAGGAGCTGGTCACCTGGACCCC GG
25	<b>Genomic hit, Accession No.</b>	CSC:AC012727
	<b>Associated ORF</b>	Genscan ORF1 predicted sequences >16:43:49 GENSCAN_predicted_peptide_7 172_aa MKLLMLGTLAFFSVISATMAANKERTFIMVKPDGVQRGLVGKIIERFEQKGFKLV 30 ALKFTWASKELLEKHYADLSARPPFGLVNYMNSGPVVPVMVWEGLNVVKTGRQ MLGATNPADSLPGTIRGDFCIQVGRNIIHGSDAVESAEKEIALWFNEKELVTWTPA AKDWIYE
	>16:43:49 GENSCAN_predicted_CDS_7 519_bp	atgaagctcctgatgctcggcacaaatgttgctctgttaatctggcgacaatggcggttaacaaggagaggactttcatcat 35 ggtcaagcccgatggcgctccagcgcggtcgtcggaagatcatcgagcgcttcgagcagaagggttcaagctggcgccc tgaagttcacctggcgctccaaggagctgctggagaagcactacgctgatctgtccgcccccttctccccgactcgtgaa ctacatgaactccgccccgtggtgcccattgtgtgggaggtctgaatgtggtcaagaccggtcgccagatgctcgcgccac caaccccgcgactcgtgccccgaccatcgcggtgacttctgcatcaggtcgagcgaacatcatccacggctccgatgc 40 cgtcgagtctcgcgagaaggagatcgccctgtggttaacgaaaaggagctggtcacctggaccccgccgccaaggactgg atctacgaatag
	<b>Drosophila Gene Hit</b>	rescue sequence and TBLA; abnormal wing disc (awd) (X13107)
45	<b>Human Homologue</b>	BLASTX with awd and TBLASTN with ORF1: tumor metastasis inhibitor nm23-H2 (A49798) non-metastatic cells 2, protein (NM23B) (P22392) and nucleoside diphosphate kinase B.

- Drosophila* EST      several including LP05977 ( AI257573 similar by TBLASTX to X92956 B.taurus mRNA for nucleoside diphosphate kinase (NBR-A)
- 5    **Annotated *Drosophila* genome genomic segment**      AE003779  
**Annotated *Drosophila* genome Complete gene candidate** CG2210 - awd abnormal wing discs nucleoside diphosphate kinase
- 10    **Human homologue of Complete gene candidate**      gi4505409  
1A5C3F84D7AD272C  
[ref]NP\_002503.1| non-metastatic cells 2, protein (NM23B) expressed in [Homo sapiens] (1.90E-61)
- 15
- Putative function**      human nucleoside diphosphate kinase, transcriptional regulation of c-myc expression.a candidate suppressor of tumor metastasis
- 20    **Confirmation by RNAi**      Only wild type profiles observed

**CATEGORY 4: ANAPHASE DEFECT****Example 31 (Category 4)**

	<b>Line ID</b>	1132/8
5	<b>Category</b>	Mitotic defects in brain: anaphase defects (overcondensation, high polyploidy, some lagging chromosomes)
	<b>Reversion</b>	?
	<b>Map Position</b>	86F3-6
10	<b>Rescue ID</b>	2C3E
	<b>Rescue Sequence</b>	GGCCGGAGGTACCATTTTGGTAGGACCGTTTTTCGGGCCAACGAAAATACCAC AAGACGGCAGCGATAATAGTGTTTTTTGCTTCAAATGTAGTATGGCTACGCAA CTCACATATGGTTAAGAACTTCGCTGTTTATTTGGTGGTTAACTAGCTAAATA 15 CAATAAGAGTGGCAACGCCGTCACGTTTTCTACATGTATTTTACTTGGCGTAGT GCGCCAAGCTTATAAACCACAGTTGGGCGGTTCTTTTGAATTGTTTAAATTTACA CCCCACTATGAACTTATTAGCCTTCTTTATTTATTTTATATTTTATTTTATTTAGGA AGAATACGTTTACTCAAGGTTTCGCAGCTTGTCAATCAGTATTCGCAAAATATCA ATAATAAAAGGCATCAATTTTCCAATCAGCAGTTGAAAAGAACTCCCCTCGAC 20 ATTTGAACAAAATGCATTTTGGGTGATTATAATTTATTAGAATTTTATTGAC TTAAGGTAAATATAAATAAAATATTATTCAAGTACAAAGGTATATATACTCAT TAATANTATTTGGATTCAAGGAAAATATATTTCAAATGGCGGGGGTTTAATA AAACAATTTTCAAATTAAGG
25	<b>Genomic hit, Accession No.</b>	AC007805
	<b><i>Drosophila</i> EST</b>	several ESTs including LP09688 (AI295922)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003693
30	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG6929 - Lk6 kinase
	<b>Human homologue of Complete gene candidate</b>	gi4505191 DB39E49EC0BED990  ref NP_003675.1  MAP 35 kinase interacting kinase 1 [Homo sapiens] (6.20E-113) and gi9994197 551A82FA3D09FD58  ref NP_060042.1  G protein- 40 coupled receptor kinase 7 [Homo sapiens] (1.70E-106)
	<b>Putative function</b>	Protein kinase associated with microtubules

**Confirmation by RNAi**  
cells

Complete loss of G1 and G2/M indicating fewer cycling

	<b>Line ID</b>	483/19
	<b>Category</b>	Meiotic defects in testis: segregation defects
	<b>Reversion</b>	?
	<b>Map Position</b>	86F
5		
	<b>Rescue ID</b>	H2S
	<b>Rescue Sequence 1</b>	CTCCGGCCACACGGATGAATTCGTCGTCATTTCGTCGGAATCATTTCGAACTTTG AAAATGGATCGGTAGCTGGGAAGGAACTTAAAGCGAAATACGCAAAGAAA 10 ACGGCTTTTGTCCGCTATTTCAGCGATTTTTTTTTGTGTTGTAATCAGCAGAGGAA ATTTTAACGACCAACTCCACCGCCACACCAGCCATCTCCAGCAGCCCCGGAAA ATAAAATAGAACTAAATTAACGCCACCATCACTACAACAACCATCTCACCAAC AACTACAAGAGCAACAACCACAGCAACAGCACTACTGCACCAAGCCCACAAA GAAGAGGTGAAACGCAATAATCGA=CAATACCCGAAGAAAAAAACAAAAAA 15 ATATCGCAGATAACCGAAAAAAGCGGTGCAATAGATAAAACCCCATTTTTTGCT TGAGCTTTTTTCGCCTGTGTGATGAGAGAAATCAGCAGCAGCCATCGATTACA ACAACAACAGCAGCCACACCAACGACGACTCACCACCAAACGAAGAATAATA ACCAGCGGANAGCGATAGATA
20	<b>Genomic hit, Accession No.</b> <b><i>Drosophila</i> EST</b>	CSC:AC018284 several including GH28825 (AI517767), LP04213

Other results same as 1132/8

**Example 32 (Category 4)**

	<b>Line ID</b>	1422/14
5	<b>Category</b>	Male and female sterile, small wings, meiotic defects in testis: segregation defects, elongation defect
	<b>Reversion</b>	NR
	<b>Map Position</b>	90B4-8
10	<b>Rescue ID</b>	2F1E
	<b>Rescue Sequence</b>	GGCCAGCTGCTCAAACATTCTGCAGCTATTTGGCCGCCAGCGAGTAGAACGAT ATTGCCAAATATTTTATAATAGTAACCAATACGTTACCAGTATGACCGCGCCG ATAACGATAGAAAATACCACACGGTCTAAAAGTAAATACCATTTGGGGTATTC 15 CCTAATCTTTTGAATTATTTACCGTTAGGTTTCGGTCGTTTTTTTTTGTGCAGCTG TTCTTTGTATGAAACGGATTAGTAATTTTATTTGTTGTTTTTGTGCATTTTTGCA TATTAAGCCTTGAACATGCCTTAAATCGTTAAAATAGATTATAAGAGGGA TGGACTGTTTGTAAACCAATTGGAAAATTTGTAATCGCTGGTAATAACTAT CGAGATAAGCTTAATTATCGCTGTTTTCTTTGTATCTAGTTATAAATAATAATA 20 ATAAACTGGTAATTAACAAAAGTAAAAAGTTACTTAAGTTATACAAAAATAT TTAGTTATTGNATTCAATAATAAGATGGTAATAATAGATGGTAAGATAGTAAT ATTTTAATAATTGAATTCATCACACATGCTGGTGCACGTTCCACAACCTACAA TCAAACGAAA
25	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003718
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG7623 - novel with homology to UDP-galactose transporter.
30	<b>Human homologue of Complete gene candidate</b>	2136348 UDP-galactose transporter related isozyme 3 - human >gi 1669564 dbj BAA13527  (1e-36)
35	<b>Putative function</b>	sugar modification protein

**Confirmation by RNAi**      **Slightly reduced G2/M**

**Example 33 (Category 4)**

	<b>Line ID</b>	1479/10
	<b>Category</b>	Mitotic defects in brain: anaphase defects (overcondensation, anaphase bridge, metaphase with swollen chromosomes and bipolar spindle)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	69F3-7
	<b>Rescue ID</b>	2D6E
10	<b>Rescue Sequence 1</b>	CCACGGGCAAATGTGGTCCGGAGGTCCACGACAACGTGCCGCTGACCATATC CCAGATTGAGCGCGCAACTCAGGATCCGGAGAACGAGAATGTGTTTCATCACA GACGACGTGCATCCGATTCACCTTCTGCACCTGCATCATCTACGCCCTTTGTAAC GGCAATGGAACGCACAACGAGTCGTTTCATGAAGTTCATGATCGATGATGGCA 15 CCGGCTCCCTGGAGGCCAGCATCACCAAAAAACCCTTCAATGGACGCGTGATC AGCAGCCTGTACAGTGAAGCCAGTTCGCTGGCCTCGTCCGAGGCCTACAAGA GCATTGCCGTGAGCATGATGCGGCTGCTGCAGGTCTCCATGGAGTACATTGAT CCCACGCGCATCTCGAGGGGCCACAGCCTATTCCTGCGCGGTCTCGGAATAG GTTCCGCGGCAAGATGGGTCTGGACGCTTTTCAGTTCTTCATAGACAGCGGCC 20 GATCGCGGAATATGGAAATTGGCTTCGTGGACTACCTAACCGACTGGCAACG AAGGCATAAAACAATGCAAAATAC
	<b>Rescue ID</b>	2D6P
	<b>Rescue Sequence 2</b>	GCCCCGTGGACTTTTCACTCTGTTGATTCTTGCGTATCACGAAGTTATCCAGCTG GCTTTCTATGTCCTCGAAACTCTGATTAATAATCCATTCTATTTGCTTAGTCTGC GATTTCAAAGGGGATTTCTTTATTGCAGTGCATTTTGCATTAGCGCCAAAAAA AAAAAAGTTGTGAGCATGGGCGTAGACTTCGTATTTTCTTACAAATAATATTA ATTAAAATTAATTTTGTGAGCAATTTTCACACAATTGTATTATAAGTTAAACC 30 AGGGTCACATTAATTTGCAGAACCGCGCAATATTTTCTTTTAAACCCCTTACA AATTTTCAGTTGTTTGTGACTACGCCCTGCTAATTTTACTTATTAAATTCAA GTCTAAAAACATTGTCACCAGATAATACGAGTATACTATATGGACAAACGT AAAATCGTTAATAGAATATATATTCAACCATTATTTACCACCGAGAGAAA TTCATTTGCACAAAACGCCAGGTTGGCAGCACCATCATTGCGCACAGCAAGTG 35 GGCAAACCTCGTTGTATCGCTTG
	<b>Genomic hit, Accession No. AC007328</b>	
	<b>Associated ORF</b>	
40	Genscan ORF1 predicted sequences >17:42:01 GENSCAN_predicted_peptide_2 1507_aa MKLAPT VKLNNGYEMPILGLGTYNLKKSRCEAAVCHALEMGYRHIDTAYLYRNE GIIGKVLAKLIGDQKLKREQVFLVTKLWDIYHEPKMVKYACDMQLKLLGVDYID LYLMHSPVGVVDYISDEDLMPHENGQLRTNDVDYVD TYRSMEQLVHLGLVRS LG LSNFNANQLKRLLENCQIKPANLQIECHPELVQVPLIELCKFHNITVVAYSPLGRSQ 45 TCNPLPDYYTDSKLLALAAKYGKTPAQIILRYLSKDNEGEAAVKHAIDVGYRHID TAYFYQNEAEVGKAIRD KIAEGVVKREDIFLVTKLWNIFHDPERVEGICRKQLSNF GLDYIDL YLMHMPVGYKYVDDNTLLPKNEDDVLQLSDVDYLD TYKAMEKLVKL	



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5 KVAEDGAPKPATNATAATATATNEQVGEKVEGVHTLNGETDKKDDSGNETGAG  
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 15 agtttcccacttgccggcgcatcatccgctgtgtgggagccgtgcccctggccacgccacctggtggcgccctgctggagcc  
 ggtggtgcatgcagccggcgcgagtggtgagcagctatggcagtgatggcaacatgagctcaatcccaatagcagcaaca  
 gcaacaccccccacagcaatggccacaataccaacagcggcgagtggtgagtgccgggagtagtgccggaagtggacgcctctc  
 cctgccggcactttcgggattccgggaagttagggacagccgctcccagacgcagatgccaatcgatgatagatacgaagc  
 cgaggacagcagtgacgagcagtgaccagccgaagtccggcgcaatcgaccaccttcagtcggagcagctggatgag  
 20 ctggagaaggagttcgacaagtgcactatccctgcgtgaatacccgcgagaaactggccggccggacggcactgagcgagg  
 ccaggggtcaggtttgttttccaacagacgagcgaatggcgccgaccagcgggtcaactgatcaagcagcgcgactcg  
 cctcgacatcgagctcaccacgcccgttggtcaatccggtgtcagtcgggtcagtcgaatccagttccagttccagttcagtt  
 ccagaatctgccaacagaagcagccatccgtacagcaccagcaacatgtgcaacaccagcagcagcagcagcaaacgctc  
 aaccgtgcaacaccatcaatccggcgagcaaatgagcagcaaaaccagcagcgtcagcagcaaccagcacatggaagagc  
 25 cagcagcggcggtggccactgcctcaccacagcatcagctccattatcaatggcggtgagaacagtgcatcttcgctctgcc  
 catgaccttgccgatgccatgaccttgcccacggcatcgcgcgcccttcgcgctcagcttcgccgccagtcacatagccaa  
 gacgcttctcggttctccagatccagatccagccaccaaccaccaaccagcataagcccagccaaatcgcgagttcctcaat  
 gaagcctgcagctccgagcatctgtccagaatcgacaacggcgcaacaaccgcagatactcctacagccaaatcagcaatg  
 30 tgcgtgcatcgagaaaaaggaggggccatggagtgatgtga

**Drosophila Gene Hit** BLASTN with rescue sequence 2: Histone acetyltransferase GCN5  
 (AF029776) very small match at end, TBLASTN with ORF1:  
 middle domain histone acetyltransferase GCN5 (AF029776).  
 Genomic matches histone acetyltransferase

35 **Annotated *Drosophila* genome genomic segment** AE003541  
**Annotated *Drosophila* genome Complete gene candidate** CG4107 -Pcaf /GCN5 histone  
 acetyl transferase  
 transcriptional activator  
 40 protein  
**Human homologue of Complete gene candidate** gi6382076  
 72F516F8BD10CD0C  
 [ref]NP\_003875.2] p300/CBP-  
 associated factor [Homo  
 45 sapiens] (1.20E-197)

**Putative function** Transcriptional activator

**Confirmation in RNAi**      Only wild type profiles observed

**Example 34 (Category 4)**

	<b>Line ID</b>	184/5
	<b>Category</b>	Mitotic defects in brain: Anaphase defects.
5		(overcondensation, aneuploidy, some lagging chromosomes and breaks)
	<b>Reversion</b>	R
	<b>Map Position</b>	71B
10	<b>Rescue ID</b>	C4E
	<b>Rescue Sequence</b>	
		CTCGAGCAGATGTGGGACGAGCTGAGCGGAGCGCACAACTGCCAAGTAAGT GGAGCATGTGGATGAAAGGAGTTCCCAGAACAGTGTTGCCAACCAAAAAAAAA AAAAAAGTTAAAAAGTTAATTTTAATAGTGTAATAAATATGAATTAAATTAA 15 ATTTTATGTAAACAGTATTAGCTTTACATGAGATTACCAAATTGTGAGTGTCT GTGTTTGTCTTTTAAAAACTTTAAAAGCACATAAAGAAATATATTTTAAA TTTAATTAATAAGTTCGTAAAAAGTAAAAGGTAGCTAAATTAAAAAGTTTCCT ATTCAAATCAGATTTGGCGAACAAAGAGCCAAGTTGGCAACACTGACAAATGA CTCCAAGCGCGAACAAAGCGATTTCTATCGTTATCCCACTCTCTCTCCAGAG 20 ATCGTTCTCAAGGCCAAATGGAAGGGACTTCGAGACAATTTCCGTGTGGAGTC AAAAGGATCCGGCGGCCGAATAACGG
	<b>Genomic hit, Accession No.</b>	CSC:AC019852
25	<b>Associated ORF</b>	
		Genscan ORF1 predicted sequences >22:43:26[GENSCAN_predicted_peptide_2 1003_aa MAPKKSTIVLNVEQFIHDIERP AIWNRNFHCNKAFLQMWDELSGAHKLPKIVL KAKWKGLRDNFRVEYKRIPRADNGDFMVDPATFESKWLHYYALLFLTDHMRHR LPKNEQDQSFYFSQSEDCEKTVVEPDLTNGLIRRLQSDDEDYDEEEMEADGEAS 30 EATMEETMPTPPAAHQMNQVSTTPLATGALRAQEEAHQHALIKAGLLRAQLMEL EKEAEDLSRKPPPPQMTSPVAPSLQVLVEPPAAHCSPPPMVTTTSAQVQQPGSA AVLAPATTTASVSSNGAPMGGKRSVSPPLYNKAHHPLATLAAHLAAKDRN EDFGPTSAVGGNGDHLSTQHSYANGLIPALKLRPRLSEDSNFNGSSTMDTPLVP EDDDYHYLLSLHPYMKQLTAAQKLRIKTIQKLIFKELYKEDLEESNLDREVYVL 35 DDGAEVDLDLGN YERFLDVT LHRDNNITTKIYKLVIEKERTGEYLGKTVQVVP ITDAIQEWVERVAQTPVQGSSKPQVCIVELGGTIGDIEGMPFVEAFRQFQFRVKRE NFCLAHVSLVPLPKATGEPKTKPTQSSVRELRGCGLSPDLIVCRSEKPIGLEVKEKI SNFCHVGPDQVICIHDLSIYHVPLLMEQNGVIEYLNERLQLNIDMSKRTKCLQQ WRDLARRTETVRREVCIAVVGKYTKFTDSYASVVKALQHAALAVNRKLELVFIE 40 SCLEETLHSEPSKYHKEWQKLCDSHGILVPGGFGSRGMEGKIRACQWARENQ KPLLIGICLGLQAAVIEFARNKLGLKDANTTEIDPNTANALVIDMPEHHTGQLGGT MRLGKRITVFSDGPSVIRQLYGNPKSVQERHRHRYEVNPKYVHLLQGMRFVG TDVDKTRMEIIELSGHPYFVATQYHPEYLSRPLKPSPPFLGLILASVDRLNQYIQRG CRLSPRQLSDASSDEEDSVVGLAGATKSLSSLKIPITPTNGISKSCNGSISTSDSEGA 45 CGGVDP TNGHK

>22:43:26|GENSCAN\_predicted\_CDS\_2|3012\_bp  
 atggcgccaaaaagtcaccattgtgctcaatgtggagcagtttattcacgacatcaggagcgcccggccatctggaaccgca  
 atttccactgcaacaaggccttcctcgagcagatgtgggacgagctgagcggagcgcaaaactgccaagatcgtgctcaagg  
 ccaaatggaagggaacttcgagacaatttcgtgtggagtacaaaaggataccgcggcgataacggtgattttatggtgatcc  
 5 gggccacctttgagtcgaagtggctgactactatgcattgtgttttaactgacacatgcgtcatcgttgccaaagaacgacagg  
 atcagtcattttacttcagccagcaaaagcaggactgtgaaaagacagtggtggagccggtttaacaaacggctataatcgtcgt  
 ctgcaggacagcgacgaggattacgacgaggaggaatggaggcggacggagaggtagcgaagccaccatggaggaaac  
 gatgccacgccaccggctgcgcacaaatgaatcaagttagcaccacaccactggccaccggagctttgcgagcccaagaag  
 aggcacatcagcagcgttaattaaggcaggattactccgctcagttgatggagctggaaggaggcggaggacttgagca  
 10 gaaagccacctcggccacagcaaatgacatctccagtggcaccctcactacaagtgtagtggaaaccaccagccgacactgtt  
 ctccacgccaatggtgaccaccacatccgcacaagtacaacaaccgggctcagcagctgttctggcgccggcaacgaccaca  
 tcgcgctcatctgtatcctcgatggagcgcaatggcgggcaagagatctgttcgccaccgcctctatacaaaaagcacacc  
 atccgctggccactctggcagcagcacatcttggcggcaagaccgaaatgaggatttcggaccacctctgtctaggaggaa  
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 15 ggatagcaatttaattggttctcgacaatggacactccgctcgtaccagaggacgatgactaccactactgtcagcctacatcc  
 gtacatgaagcagctgaccgcagcccagaagctgcgcatacgcaccaagatacaaaagctcatctcaaggaaactctacaaga  
 agatcttgaggagtcacaacctagatcgcgagggtttacgttttgacgatggcgccgagggtgagctggatctgggaaactatgaa  
 ggtttttgagtggtaccctgcatcgggacaacaacataaccaccggaaaaatttacaagttggtcattgagaaggagcgactggc  
 gagtacttgggcaaaacggttcaagttgtccacacatcactgatgccattcaggaatgggtggagcgctggccagacacc  
 20 gticagggatcttcaagccacaggtgtgcacgtggaattgggaggaacgattggtgacatcgaaggcatgcttctgtagagg  
 ccttcgctagtttcagttccggtgaaagagagagaactctgtttggccatgtgtcgtggttccgttgccaaaggctaccggag  
 aaccaagaccaagcccacacaagtctcggtcagagaactgagaggatgtggcctgagtcgccgatttgattgtctgccgatcgga  
 gaaaccattggactggaggtcaaggagaagatcagcaactttgtcatgtggggccggatcaggtgatgacccacgatttga  
 actccatttatcatgttccgctgctgatggagcagaatgggtgttgaatacctaaatgagcgccctacagcttaatacgcacatgagc  
 25 aagaggaccaaatgcttgcagcaatggcgagattggcgctgaacggagaccgttcgccgtgaagttgcatcgccgctgtg  
 ggaaagtacaccaagtacggattcgtacgcctcgtagttaaagccctgcaacatgccgcctggcagtgaaatcgcaaaactgg  
 aactgtctttatcgagtcgtgcctgctggaggaggaactttgcatctgagccagcaagtaccacaaggagtggcagaagct  
 atcgatagccatggcaccatagtcctccgggtgattcgggtccgtggaatggagggaagattcgtgcatgccaatggcgcgga  
 gagaatcaaaagccattgcttggcatctgcttgggtctgaagcggcggtcattgaattcgacgaaataaacttggctcaaggat  
 30 gcaaacaccacagaatcgatccgaacacagctaattgcttgcacatgataccagagcatcacacgggtcaattggcgggc  
 actatgcgcttgggcaagcgaataactgtttctctgatgtgcctagtgtcattcgccagttgatggcaatccgaaaagcgtgcagg  
 agcgtcatcggcatcggtacgaggttaatcccaatacgtgcatctgctggaagagcaaggcatgctgatttggggcaccgacgt  
 cgacaaaactaggtggaatcattgagtcagcggtcatccctactttgttgcacccaataatcatccagagtactgtcgcggcc  
 tctgaagccgtcgctccttctcggcctgatcctggcctcagtgatcgattgaaccaataatcagcgcggttggcgctgtcg  
 35 ccccgccagctatccgacgcatcctcgatgaggaggacagtggtgtggcgttggccggagcaacaaaatcgtgagctccttg  
 aaaattcccaattaccccacaatggaatatcaaaaagttgcaatggtagcataagcacttccgacagcgaagggtgcctgcggag  
 gcgttgatcctaccaatggccataagtaa

Human Homologue TBLASTN with ORF1: CTP synthase (CTPS) (NM\_001905.1)  
 40 *Drosophila* EST LD27370 (AA941993)

Annotated *Drosophila* genome genomic segment AE003532  
 Annotated *Drosophila* genome Complete gene candidate CG6854 - novel protein,  
 possible CTP synthase?

45 Human homologue of Complete gene candidate gi4503133  
 C33BD849A0044697  
 |ref|NP\_001896.1| CTP

synthase; cytidine 5-prime  
triphosphate synthetase  
[Homo sapiens] (8.40E-217)

5

**Putative function**

Enzyme important in the biosynthesis of phospholipids and nucleic acids, and plays a key role in cell growth, development, and

10

tumorigenesis. The region of the human gene is the location of breakpoints involved in several tumor types

**Confirmation by RNAi**

Loss of G1 and G2/M peaks indicating fewer cycling cells

**Example 35 (Category 4)**

- 5    **Line ID**                      225/27  
      **Category**                  Meiotic defects in testis: segregation defects  
      **Reversion**                  NR  
      **Map Position**               90D
- 10   **Rescue ID**                  2D2P  
      **Rescue Sequence 1**
- Rescue ID**                  2D2E
- 15   **Rescue Sequence 2**  
      GCCTGAACTTAAAACGCTGCCTTCGGCTCTCGCTCGGCACTCGCTCGGCTGCG  
      ACGTCGACTGCGACGCTGGCAGCGACAACAACGATTGGCCTCTCTCATTCACT  
      TACCTCCTCTCTCTCTCTCGCACTCTCTCTTAGCGGTGAGAGAGTGTTCCTC  
      ACATTTGTTTTGCTTTTGCGGTTGCGCAATGGCCCCCAAAACGAAAAGAGCG  
      20   CGCAAGAGCTAGCTCCACAGTGGATCCTAAGAGAACGGTCCCTGTGGACTCC  
      ATCTAGCTAAGAGAAACGCACTTAGTTAGTTTCTATTTTGGTTGTTAAGTAC  
      TGCTAGCTGCCTGCCAGTTGAGTGTCCGTCCAAAAACGGTGGTGGAAATGGGG  
      GTGACCACTTCAAACATGAAAGCGAAATGTCCTGAGACCCTACAAAAACTAG  
      AAATACGCGGGTGCCTGAGAGAAATTTTTATTTCAAGTAAATTGGCAGAGG  
      25   CTACATTTTGAATGTTTACAATGAAAATTGCTGGGGAAGCTAGTGAACAACCA  
      TTTCGCCATAATTTACACTATCTAAGCTTTTATTTTATAGCCACATGATATATGC  
      ATGCA
- 30   **Genomic hit, Accession No.** AC008361
- Associated ORF**  
      Genscan ORF1 predicted sequences >20:36:39|GENSCAN\_predicted\_peptide\_2|515\_aa  
      MSSTIRLQTSSCQCKLYKYERHPNKPQLPTIPNYPCEILHIDIFALEKRLYLSCI  
      35   DKFSKFAKLFHLQSKASVHLRETLVEALHYFTAPKVLVSDNERGLLCPTVLNLYR  
      SLDIDLYYAPTQKSEVNGQVERFHSTFLEIYRCLKDELPTFKPVELVHIAVDRYNT  
      SVHSVTNRKPADVFFDRSSRVNYQGLTDFRRQTLEDIKGLIEYKQIRGNMARNKN  
      RDEPKSYGPGDEVFVANKQIKTKEARFRCEKVQEDNKKNRNGKAAGGKGKTR  
      RVARGAQIYQNWAI CRNLF LFLSLACCRVCKVCDIVVEFRKGTNAVNVQIREAI  
      40   SHVFHKEDIVIDVQESKEWCIWTDDQVQSPLPELENLWHELWIGPSHAYLIDQIVD  
      LFENLLEKYNVQVVDVVRFNFLHRA LVVVIISGIIIIIMIGVSGGQRTNAFHHRS  
      QRSAIGGDPQQKDSAVQQVQARSSDAFCQIPHRSPRFPGRSQLIPKNREILRNASA  
      TKNLLFRIRSQ
- 45   >20:36:39|GENSCAN\_predicted\_CDS\_2|1548\_bp  
      atgtccagtagcatccgtctgcaaactcctcatgtcagtggtgcaaactctacaagtagagagacaccctaacaaccaaacta

caacctacgccaattcctaactacccatgtgaaatacttcacatcgacatcttgcgctcgaaaaagggtatacctaaagttgtattgac  
 aaatttagcaagtttgccaaactttccatctgcagtcacaaagcatctgtgcatttgcgagaaacttggaggaggccctacattacttc  
 accgcccctaaggctctgttccgataacgagcgagggtgttatgcccacagtgctcaactatctcggctctagatcgcgatct  
 gtattatgctccaaccagaagagcgagtaaatggtaagtcgagagattccactctacgttcctagaaatttatcgttgccctaaa  
 5 gatgagctccctacctcaaacccgttgagctggtacacatagcagtgaccgctacaacacttccgttcactcggtaacgaatcg  
 aaaaccagcagacgttttttcgaccgctcgaagggttaactatcagggtctgacagatttccggcggcagactttagaggacat  
 caagggttaattgagtataagcaaattagaggtaatatggctcggataaaaaataggacgagccaaagtcttatggccggga  
 gatgaagttttgtgcaaataagcaaataaaaaacaaaggaaaaagcgaggttcagatcgaaaagggtacaggaagacaacaag  
 aaaaatcgcaacggaaaagcgccgggtggaagggggaaaactcgagagtagcccggtggagctcagatttatcaaaactggg  
 10 caatctgccggaatctgttctgttctgtcttgcctgtccgagtggtgtaaagtgtgtgataatgctgtagaattcagaaaaggaa  
 ccaacgccgtcgtgaacgtgcagatccgtgaagctatcagccatgtgtccataaagaagacatagtcacgatgccaggagtc  
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 tagccatgcgtacatgatcagatgtcgcgtcttctgaaaatctgctcgaaaaatataatgtgcagggtgtcgtatgttcgggt  
 caatttctccatcgctctcgtagtcgtgatcatttccgggtatcatcatcattatcatcatgatcgcggcgttagcggcgcca  
 15 aagaacaaatgcctttcacaccaccgatctcagcgatcagcgatcggcggcgaccctcaacaaaagattcagcgggtgcaaca  
 ggtgcaggcacgatcttcggatgccttttgccagataccccaccgatctccagggtcccaggcgagccaacttattccgaagc  
 caaatcgagaaattctcgaacgcgagtgccacaaaattattgttcgaattcgcagccagtga

**Drosophila Gene Hit** BLASTN with rescue sequence: couch potato (Z14974).  
 20 **Human Homologue** BLASTX with couch potato: RBP-MS/type 2 (RNA binding motif family)(D84108)

25 **Annotated *Drosophila* genome genomic segment** AE003720  
**Annotated *Drosophila* genome Complete gene candidate** CG18434 -couch potato RNA binding protein  
 30 **Human homologue of Complete gene candidate** 2224621 dbj|BAA20798| (AB002338) KIAA0340 [Homo sapiens] (2e-19) and Ensembl predicted peptide Gene:ENSG00000070877 Clone:AC009710  
 35 Contig:AC009710.00004 (predicted unknown protein)

**Putative function** Possible RNA binding protein



**Example 36 (Category 4)**

**Line ID** 238/37  
**Category** Meiotic defects in testis: segregation defects, multi-stage defects  
 5 (P1-02/17)  
**Reversion** ?  
**Map Position** 70D  
  
**Rescue ID** I7E  
 10 **Rescue Sequence**  
 GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC  
 TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG  
 TCTTCGCTCCATTTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT  
 GATTAGGACACGGGCTGCCTGAGCTTGACGTACAATGGTCGGACGCACTACG  
 15 CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG  
 GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCCGG  
 ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG  
 TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGA  
 GAATGATCTGGTCAAGTGTGCGCTCATCGCTGACGTTCTCAACCTGCGCAGCG  
 20 TCCACGTTACCCCCGTCTCGTCCAAGGACTGGGAGATCATAGTGAGTGACGGT  
 TTCGCCTGCTTGGCGGCGTGG

**Genomic hit, Accession No.** CSC:AC017664

25 **Associated ORF**  
 Genscan ORF1 predicted sequences >15:26:30|GENSCAN\_predicted\_peptide\_1|1819\_aa  
 EMVQAKDPPSHYLSKLRTYLDPKASRSHRLYLFYFLCQKRKMVGESTSTQVLRD  
 LEISLRTNHIEWVKEFLDDTNQGLDALVDYLSFRLQMMRHEQRLQGVLCASEERL  
 NLTNGGDGGEIVMGNSSSVSPGGGGGLLSHGNSTGHGLANGTLDNRQQHTMSYG  
 30 FLRPTIADALDSPSLKRRSRHIAKLNMGAAATDDIHVSIMCLRAIMNNKYGFNMVIG  
 HREAINCIALSLIHKSLRTKALVLELLAAICLVKGGHEILGSFDNFKDVCQEKRRF  
 QTLMEYFMNFEEAFNIDFMVACMQFMNIVHVSVEDMNYRVHLQYEFTALGLDKY  
 LERIRLTESEELKVQISAYLDNVFDVAALMEDSETKTSALERVQELEDQLEREIDR  
 NSEFLYKYAELESESLTKTEREQLAMIRQKLEBELTVMQRMLOHNEQELKKRDT  
 35 LLHTKNMELQTLRSLSRASSGDGSLANGGLMAGSTSGAASLTLPMPMPMPASP  
 TASSAAPPPPPPPAPPAPPPPPGFSPLGSPSGSLASTAPSPPHAPPMLSSFQPPPPVA  
 GFMPAPDGAMTIKRKVPTKYKLPNLNIALKPNQVRGTIFNELDDEKIFKQIDFNE  
 FEERFKIGIGGALRNGSNGTEVDGSLQSSKRFKRPDNLVSLLEHTRLRNIAISRRLG  
 MPIDDVIAAIHSLDLKKLSLENVELLQKMVPTDAEVKSYKEYIIERKDQQLTEED  
 40 KFMLQLSRVERISSKLAIMNYMGNFVDSVHLISPQVQSIAGASTSLKQSRKFAVL  
 EIVLAFGNYLNSNKRGPAYGFKLQSLDTLIDTKSTDKRSSLLHYIVATIRAKFPELL  
 NFESELYGTDKAASVALENNVADVQELEKGM DLVRKEAELRVKGAQTHILRDFL  
 NNSDKLKKIKSRLRHAQEAFFKECVEYFGDSSRNADAAFFALIVRFTRAFKQHD  
 QENEQRLRLKAAALAASKKENDQVLMRNKVNQKKQQA VINELKSKAHSVRE  
 45 KKLLQQDEVYNGALEDILLGLKSEPYRRADAVRRSQRRRIDNNRLSRTLEEMDCL  
 HENDLVKCALIADVLNLRSVHVTVPSSKDWEIHELSTEKISGSVLEQTRIVNSTQILI

- VWINKSMQVALTVDRCLKPHMNYGRIDHNTELVVAPNLKGLTNGTSNGVIEENT  
KLSRSKTTAQQKDELTEKLTPLTHSSTVSNVKNTIQRNKRQDHMERLKKDLRRES  
SRSFEFRVIRGLWREQAQESDVFNKGHLPEFFDLDFYCMHTAADKDYVVRVR  
TVEDDIEDDLPETIHPSIELNANLMKLLGIKELERVVLRPKTTVVNFVEKIELFANK  
5 KTHYKIMENAFKRFVIERTQHKPMLFNQEEVVRLEDDLVTVGILPEHFRYCVVD  
AQFLKESKIYAADLVRPVGEIIEETPPTSPLSVQDLIQLPEYDKIVDQVVQELRMN  
LCLSDNSVMRQCNVLLAGASGTGKTVLVERILDQLSRKPDYCHFEFFHGSRSKG  
RKTESIQKDLRNIFTSCLQHAPAIIVLENLDVLAHAAGEQSSQDGEYYNRMADTV  
YQLIVQYTTNNAIAVIATVNELQTLNKRLLSSPRGRHVFQTVARLPNLERADREILR  
10 ELCSHINVAKDDLKFKSNLTEGYRKCDLVQFVERAIFYAYRISKTOPLLNDQLI  
ESLEHTNSYCLQGIQSNQRTGNDADANEMRVEELPGLESVVGVLEEVLMWPSRY  
PTIFNASPLRNQAGVLLYGPPGTGKTYLVSQATSWNLRISVKGPPELLAKYIGQSE  
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- 15 >15:26:30|GENSCAN\_predicted\_CDS\_1|5457\_bp  
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20 ggcatggtgcggtgagatagtgatgggaacagtagttctgttagtcctggtggaggtggtggttactatcacatggaacagtac  
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25 atcattttgggtcgttcgataattttaaggatgtgtgccaggagaagcgacgcttccaaacgctcatggagtagttatgaattcga  
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gcttgaggatcaacttgagcgagaaatagatcgttaactcagagttcctctataagtagtcggaattagatccgagagtgtaacgt  
30 gaaaacggaacgcgagcagctgctatgattcggcagaagctggaggaggaacttacagtatgcagcgaatgttcagcacaca  
acgagcaggagctgaagaaacgggacacactgctgcacacaaagaacatggagctgcagacgcttgcgttcctgccacga  
tccgctccagcggcgatggttctgctgcgaatggtggcctcatggtggttcacatcggggcagcctcttaacattgccacc  
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accaccggcggttcagtcgctggcagtcggcggcagcctagcctcgacagcgccatcgccgccacatgccccgcc  
35 atgctaagctccttcaaccgccaccgctccagtgccggctttatgcccgtcccgatggcgccatgacctcaaacgaagg  
tgccactaaatacaagttgccacctgaactggatagcactaaagcctaatacaggtacgtgtgtaaatattcaacgagctggatg  
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gtaagaacattgcaatctccgctcgaagctgggtatgccattgatgtatgcgcgccattcatagctggacctgaagaa  
40 actttccctggagaacgtcagctgctgcaaaaaatggtgccacggatgccgaggtcaaatcctacaaggaatatatcatcgag  
cgcaaggaccaacagctactcaccgaagaagacaagtttatgctgcagttgctgcgtgaggagctatctcgtccaagctagcca  
ttatgaactatattgggcaatttgcgacagcgttcatctcattagtcgcaagtgaatcgatagcaggagcgtcgaattccttaaaa  
caatctcgaaaatcaagcggttttgaaattgtcctggttctggcaactatctcaacagcaacaaacggggaccagcctatgg  
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 tgcgcgagaaaaagctgctgcagcaggacgaggtgtacaacggagccctggaggacatcctgctcggcctgaagagcagagcc  
 gtacaggcgggcgatgctgtgcggcggcgcagcgcggaggatcgacaataatcgtttatcgcgcaccctggaggaaatgg  
 5 attgtctgcacgagaatgatctgggtcaagtgtgcgctcatcgctgacgttctcaacctgcgcagcgtccacgttaccctcgtcgt  
 ccaaggactgggagatcatagaacttagcactgaaaagatatcgggcagtgctggaacaaactgcatagtgaattcaacgca  
 gatccttattgttgattaataagtcgatgcaagttgcgctgacagtggatcgtctgaagccgcacatgaactacgggagaataga  
 tcacaatacggaaactcgtggtggcgcccaatctgtacaagggtctgaccaatggaacttcaaatggtttatagaggaaaacaca  
 aactctccagaagtaaaaccactgccaggtcaaggtgatgactgactgaaaagttaacaccgttgaccattctccacggtgtcc  
 10 aatgtgaaaaatactattcagcgttaacaagcgtcaggatcacatggagcgtcttaaaaaggacttgcgcgcggaagctcgcgta  
 gcttcgaattctgtcattcagaggtctatggcgggagcaggccaggatcggtgtttgtgaacggaaagcatctgcctgag  
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 aggacgatctaccagaacacattcatccatcgatcgaaactaatgccaatctatgaagtgtcgtgggtattaaaggaattggaacgag  
 tggttctaagacctaataactaccgtagtttaactttgtagaaaaaattgagctatttgcacaagaagacgcactacaaaatcatgga  
 15 gaacgcatttaagcgatttgtatagagagaactcagcacaagccgatgctcttcaaccaggaggagggtggtcagcgctggaggga  
 cgatttactgttactgttggaattttaccagaacactttcgttattgctggtggagcgcgagtttctgaaggagtcgaagatctacg  
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 gttaccggagtagcagataagattgtggatcaggtatgacaggaaatgccaatgaatctatgcctcagtgctgacaattccgtcatgcgt  
 cagtgcaatgtcctactcgtgtgctcgggaacgggtaaaacagttcttggagcgcattttgaccagctgtcacgcaagcc  
 20 ggattattgtcacttcgagttcttcacggatcgcgaagcaagggccgaagacggagtcacatccaaaagatcttcgcaacatttt  
 taccagctgcctgcagcatgccccgccattgtgtgctagaaaacttggatgtactggccacgctgctggagagcagtcacgtc  
 aggatggagagtactacaatcgatggcgatactgtgtatcagttgattgtcagtataccaccaacaacgctattgcagtaatcg  
 ccaccgtcaacgagttgcagaccctcaataagcgattgagctcaccaaggggaagacatgtctccagactgttgcgtcgtcgtccc  
 aatttgaacgagcagatcgagagataattcttcgagagctgtgcagccatatcaatgtggccaaggacctggatcttgttaagtct  
 25 ccaacctcacggagggtaccggaaatgtgatcttgttcagttcgtggagcgtgcaatatttatgcttatcgcataagcaagacc  
 agcctcttctgaccaatgatcagcttattgagtcctggagcacacaaactcgtactgcctgcagggcattcagagcaatcaaaga  
 actggcaatgatccgatgccaatgaaatgcgctgcgagggagttgcctggcctggagtcagttgtgggagttctggaggaggtcc  
 ttatgtggccatcaagggtatccaaccattttaacgcctctccactgcgcaaccaggccggagtacttctatatgggccaccaggaa  
 cagggtaaaacctatctggtctcagttggccacatcgtggaacctgcgcatattccgtcaagggtcctgagttgctcgccaaata  
 30 tattggtcaaagcgaggaaaatgttcgaaacctgttcaatcgagctcgcagtgcccaccatgtgtgcttttctcgcagagtttgac  
 agcttggcgccgaaacgtggtcacgattccacgggggtcaccgatcagtg

**Drosophila Gene Hit** recue sequence and TBLastn with ORF1: mRNA for l(3)70Da (AJ243811)

35 **Human Homologue** BLASTX with l(3)70Da: peroxisome biogenesis factor 1 (AF026086)

**Drosophila EST** LD43687 ( AI512050)

40 **Annotated Drosophila genome genomic segment** AE003536

**Annotated Drosophila genome Complete gene candidate** CG6760 mRNA for l(3)70Da  
 - novel protein with  
 homology to endoplasmic  
 45 reticulum ATPases

**Human homologue of Complete gene candidate** 4505725

ref|NP\_000457.1|pPEX1|  
peroxisome biogenesis factor  
1 >gi|2655141 (AF026086)  
(8e-80)

5

- 10      **Putative function**      Putative member of the AAA protein family (ATPases associated with diverse cellular activities) including homologies to transitional endoplasmic reticulum atpases, and an E.coli membrane-bound AAA-type metalloprotease which degrades degrades sigma32, an alternative sigma factor for heat shock promoters
- 15      **Confirmation by RNAi**      Slight loss of G1, increase in G2/M indicating arrest in G2/M

	<b>Line ID</b>	238/44
	<b>Category</b>	Meiotic defects in testis: segregation defects, multi-stage defects (PI-02/18)
	<b>Reversion</b>	R
5	<b>Map Position</b>	70D
	<b>Rescue ID</b>	F8E
	<b>Rescue Sequence</b>	
	GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGAGCAACTTTGTTC 10 TGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGG TCTTCGCTCCATTTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTCT GATTAGGACACGGGCTGCCTGAGCTTGACGTACAATGGTCGGACGCACTACG CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCCGG 15 ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATTTGCCCGG TACCTCGTACGCTAGCAGCACCCACTTACCCTTTCTTGCCGTATGTCTGCACGA GAATGATCTGGTCAAAGTGTGCGCT	
20	Other results same as for line 238/37	
	<b>Line ID</b>	428/5
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects, segregation defects (seg-01/01)
25	<b>Reversion</b>	?
	<b>Map Position</b>	70A
	<b>Rescue ID</b>	G4E
	<b>Rescue Sequence</b>	
30	GTTCAAACGCACTTTTAAGGTGGCCTATCGGCCCATCAGGGAGCAACTTTGTT CTGCTGCCGGATCAGTACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAG GTCTTCGCTCCATTTCAGATTAGATACGCCAAAGATTAATCCGGTCAACCATTTC TGATTAGGACACGGGCTGCCTGAGCTTGACGTACAATGGTCGGACGCACTACG CCTCCTGGGCGCCACAAAAGGGCGGCGGCGGCATTAAAGACACCGAGATTGG 35 GATCAATGCCAGAGCGGCCAAGGAGATCGGTAAGCCATTACTTAACGGCCCGG ATGTGCATCGGTTGCCAATGTGCCGTAATATTGGACTCCGGCCATCTGCCCCG TACCTCGTACCTAGCAGCACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAA AATGATCTGGTCAAGTGTGCGCTCATCGCTGACATTCTCAACCTGCGCA	
40	Other results same as for line 238/37	

	<b>Line ID</b>	848/7
	<b>Category</b>	Mitotic defects in brain: cytokinesis defect. Meiotic defects in testis: cytokinesis defect. Multi-stage defects Polyploidy, no overcondensation PI-01/10
5	<b>Reversion</b>	R
	<b>Map Position</b>	70D1-2
	<b>Rescue ID</b>	G1E
10	<b>Rescue Sequence 1</b>	GGCCACCTTAAAAGTGCCTTTGAACATTCTCGTCGTGGGCGTGTGCGAATTTA GTACGCTCCTTCCTGGTTTAAATCATTTTCGCACTAAACTTCTGCTCTCAGCGG AATTTACTTTTGCTTTATTAGAGATGGGAGCTCGCGCATCAGCTGAGCCGATA CTTGCGCAACAGGTGATACAGCTGATTAGAGATGGCCCTTTTCAACTGTTCCC 15 AGCAGTGACCGCTGCCATAACCGTTTTCAAATTTACGTGAGAACAGACATAA AATAAATATTACAGCTCGTAGTAAATGTTATTCTATATTTAAAAGGAAATTGT AATAGTTAAAACTTGCAATGAATCAGTTACGTTCAAAAAAGGAAACACACTTT AGTTTTTGGCTAGTTTATTGGGTTAATAATTTTTATTTAAAATAGTTCGAGTG TTCAATATAGTCATGTAAATGTGTACAGAAAGATCCGGCATTGATATTTAAT 20 ATATCGATTTCCCTTCACTTTTCGCTCCTCGTATACCATGCTGGGGTCTTATCAA ATTTATT
	<b>Rescue ID</b>	G1P
	<b>Rescue Sequence 2</b>	AAGGTGGCCTATCGGCCCATCAGGAAGCAACTTTGTTCTGCTGCCGGATCAGT ACTACGGCGTCGTTTCGACCTATGTAAGTGTCTAAAGGTCTTCGCTCCATTCAA ATTAGATACGCCAAAGATTAAATCCGGTCAACCATTCTGATTAGGACACGGGCT GCCTGAGCTTGCAGTACAATGGTCGGACGCACTACGCCTCCTGGGCGCCACAA AAGGGCGGGCGGCGGCATTAAAGACACCGAGATTGGGATCAATGCCACAGCGG 30 CCAAGGAGATCGGTAAGCCATTACTTAACGGCCGGATGTGCATCGGTTGCCAA TGTGCCGTAATATTGGACTCCGGCCATCTGCCCCGTACCTCGTACGCTAGCAG CACCCACTTACCCTTTCTTGCCGTAGGTCTGCACGAAAAATGATCTGGTCAAG TGTGCGCCTCATCGCTGACGTTCTCAACCTGCACAGCGTCCACGTTACCCCGT CTCGTCCAA
35	Other results same as for line 238/37	

**Example 37 (Category 4)**

**Line ID** 252/40  
**Category** Meiotic defects in testis: segregation defects, abnormal spindles.  
5 (Ab-03/30)  
**Reversion** R  
**Map Position** 84E

**Rescue ID** A4B  
10 **Rescue Sequence 1**  
TACATGACTCTGCGATTTGACAAAAACAAAATTGAGTTTTGTCAAGAAAATCA  
ACTATTTTTCTGTGTTTAAAAAACCGAAGCCAACAAATCCGACCAAAATGCCT  
GCCGAAAACCTTGAGGAGCAGGGTCTGGAGAAGAACCCGAACCTGGAGCTGG  
CCCAGACGAAGTTCCTGCTTACCCTGGCGGAATACAAGCAGGATGCGGCATTG  
15 AAGGCGAAGCTTCTGGAGGCGATTGCGACGGAGAATATGGCCCCGTGGGTAC  
GAGCACATCCTGCTCCGGAACCTCGGCTTGGACCCGTTAGACAAGGATCTTGCC  
TGGCGCCGAATTGAAGGAAAAACAATCGCGTTTAAGTTGGGAGCCA

**Rescue ID** A4E  
20 **Rescue Sequence 2**  
GTCATGTACTACCAGTGTGACCCCAAAGTTATCGATAAATTATACCGCATATT  
TTAACATTGCCAAAAATACCAGAGCGATGTCCATCAAGATAGCGACGAAATT  
AGAACAGTGCAATTGCCAATTGGGAATTTGTATTTTAATTTATTTTAAATTCT  
GAAAGTAATTTTAATTTAAAAAAAACCTTGAGAGCTGTCTAGAAAAGAACTTAT  
25 GTTTCATGATAACTTTGTGCGAAGAATTAAGAAATATTTAGTTGTAAAATAATT  
GTNTGAATCTATTTTTTTTCCAATAACACGACTTATATTTTTTTTTTAAATATTC  
CGAGCTAAATCCCAAGAAAGTTAAACTCCAATCTTGGGATTTTGAAGTGCCCC  
AGAAACTCCAAATTAACACTTCCTTTTTAAATAATTGTTAAGACCCGTATCA  
CTTATGGTTATATACTGACCTCGAAAGGGCCACACTAAGGGGGGAGTTTGAAA  
30 ATTGATTTTCCTGATAAAAATTTTCGCTTGGAAAGCTACAGCATCGTCCACTGTC  
CATGTTTATATATCCTTATATTTGCCTATAAATATAT

**Genomic hit, Accession No.** AC006494

35 **Associated ORF**  
Genscan: ORF1 predicted sequences >23:00:28|GENSCAN\_predicted\_peptide\_2|389\_aa  
MPAENLEEQGLEKNPNLELAQTKFLLTLAEYKQDAALKAKLLEAIRTENMAPWY  
EHICSELGWTVDKDLLARMKENNRVEVEQLDAAIEDAEKNLGEMEVREANLKKS  
EYLCRIGDKAAAETAFRKTYEKTVSLGHRDLIVFHLIRLGLFYLDHDLITRNIDKA  
40 KYLIEEGGDWDRRNRLKVYQGVYSVAVRDFKAAATFFLDTVSTFTSYELMDYPT  
FVRYTVYVAMIALPRNELRDKVIKGSEIQEVLHGLPDVKQFLFSLYNCQYENFYV  
HLAGVEKQLRLDYLIHPHYRYVREMRLGYTQLLESYRSLTLQYMAESFGVTVE  
YIDQELARFIAAGRLHAKVDRVGGIVETNRPDNKNWQYQATIKQGDLLLNRQKL  
SRVINI  
45 >23:00:28|GENSCAN\_predicted\_CDS\_2|1170\_bp

139

atgcctgccgaaaacttgaggagcagggtctggagaagaacccgaacctggagctggccagacgaagttcctgctaccct  
 ggcggaatacaagcaggatgcggcattgaaggcgaagcttctggaggcgattcgacggagaatattggccccgtgtacgag  
 cacatctgctcggaaactcggctggaccgtagacaaggatctgctggcgcgaatgaaggagaacaaccgcgtagaggtggagc  
 agctagatgcggcaatcaggatgcggagaagaatctgggcgagatggaaagtcgcgagcggaatcttaagaagtcagagta  
 5 cttgtgccgcatcggcgacaaggctgccgcagagactgccttccgcaagacctacgagaagaccgtttccctgggtcaccgcct  
 ggacatcgtgttccatctgatccgcttgggactgtttaccttgaccacgatctcatcactcgcaacatcgacaaggccaagtatctg  
 atcgagggaaggcggcgattgggaccgacgcaaccggtgaaggctctaccagggtgtttactcgggtggcggtgcgtgactcaag  
 gcggcgccacgttcttctggacaccgtaagcaccttcacctacacgaactgatggactacccaccttcgtgcgttacaccgtt  
 tacgtggccatgattgccctgccgcgaatgagctgcgcgacaaagtatcaagggtccgaaatccaggaggtgtccatggc  
 10 ctgcccgcgtgaaacagttcctgttttctgttacaactgccaatatgagaactctacgtacacctggccggcgtagagaagcaa  
 ttgcgcttggactacctcattcatccctaccgctactacgtgcgcgagatgcgcattctgggtacacccagttgctggagtcg  
 tatcgtccctcaccctgcagtatatggccgagtcgttcggcgtaacagtgaatacatgaccaggagctggcacgctcatcgc  
 cggcgagcggtcatgccaaagggtggatcgcgttggcggtgttgagaccaatcgccctgacaacaagaactggcagttacc  
 aggcgacatcaagcagggcgatctgctgtcaaccgcatccagaagttgagccgctgataaacatctaa  
 15

- Drosophila* Gene Hit** BLASTN with rescue sequence 1 and TBLASTN with ORF1: 26S  
 proteasome regulatory complex subunit p42A (AF145308).  
**Human Homologue** BLASTX with EST and TBLASTN with ORF1: Hypothetical  
 protein KIAA0107 (D14663).  
 20 ***Drosophila* EST** several including GH17651 (AI387197)

- Annotated *Drosophila* genome genomic segment** AE003739  
 25 **Annotated *Drosophila* genome Complete gene candidate** CG5378 - Rpn7 19S  
 proteasome regulatory  
 particle, non-ATPase protein,  
 subunit S10aHuman  
 Homologue

- 30 **Human homologue of Complete gene candidate** gi7661914  
 8843E6684AE91ACD  
 [ref]NP\_055629.1| KIAA0107  
 gene product [Homo sapiens]  
 (3.40E-149)

- 35 **Putative function** component of the 19S proteasome regulatory particle

- Confirmation by RNAi** Marked decrease in G1 and G2/M indicating fewer cycling  
 cells

40



**Example 38 (Category 4)**

	<b>Line ID</b>	277/7
	<b>Category</b>	Mitotic defects in brain: anaphase defects (weak, higher condensation, some polyploidy, fewer anaphases, polyploids with monopolar spindles)
5	<b>Reversion</b>	?
	<b>Map Position</b>	71B
	<b>Rescue ID</b>	B8E
10	<b>Rescue Sequence</b>	AGTCGGCGCATGCGGAGAGAGAATCGAAAGAGAAAGAGAAGCAAAGAGAGC GACATACAGCAAAAACAATTCAAAAAGAACTGGTGAAGAATACGAAAATAAG ATAATTTTTTAAGGAAGTCGCGCTTTGATCCGTATCCGTTTTAGCGTCCAAGAT TTATATCTTAAATCGGACCTATATTTTGAGGTACAGTGAAGCTTTGATGCGCCA 15 GTCTTATATGAGTTAAAGTTTTAACGATTGAAAGACACCCCTGAGCTGCTCAT TATATTTCAATATTTATAAACAATCTTATATCAGAGCTTGAGAGACTTGTCATGC GCCACAAAATTCCAATTCCAATTCCAATTCCGGAATAATTCACAATAATCTC AATTAACATACGTATTTTATGTTTCGTAATTTTTTAAAAATCCCAGATTCCCCAC AATTGCCATAATAATCTCGATTATGTTATTATACTCTGAGAAGTAGGAGTGTG 20 TGCAAAGACCACAAACAAATCATTAGGGGCGT
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003584
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG15383 – novel
25	<b>Human homologue of Complete gene candidate</b>	none
	<b>Putative function</b>	No homologies to indicate function
30	<b>Confirmation by RNAi</b>	Slightly increased G1 decreased G2/M indicating arrst in G1

**Example 39 (Category 4)**

	<b>Line ID</b>	284/4
	<b>Category</b>	Mitotic defects in brain: anaphase defects (overcondensation, polyploidy (with overcondensation), few anaphases, metaphase with bipolar spindle)
5		
	<b>Meiotic</b>	
	<b>Reversion</b>	NR
	<b>Map Position</b>	89B
10		
	<b>Rescue ID</b>	2C6E
	<b>Rescue Sequence</b>	GTCTACCACTAGCTCTTTGTCTTCGCCTTCTAGTCTCTCTCATCTTGGCAGCCC GTTCTAGTGCGCGTATTTTTAGTCGCAACACATTGCCCAATTGCCAGCCGCTA 15 TTTGTGTCGTCCATTTGTTCAATTCATCGGGCTCTTTTCCGATTTCAAGTGGGTGG CATTTAACAATAATCCCTGCGTTCGCTGTCCACGTCCACATTACGATACGTTTA GTGCACGGAAGAAATAAGCGTGTGGTTTCATAATATTAGCTATTGAAAAAA GTTCTTAAATTTAAGCCTCACTCGATTCTGATGCATGAAATATTATTGGATTGT AAATGAGCGTCATGTTTTGGTATACAAATCTCAAAGTAATTTAAAAATTCTCA 20 TCTTACCGTACCTTGAACCACTACCAATCATCTCAGTACAGCATTTTCAGCGAA TTTCTCACTGTGCACTACAATGCCAGGCGGTACAAGCACCTGTATTTATTTATG GTCCGCTGCCGTAATCGACTGCAGTCGCCGCTTCCCTCTCTCTTTTGCTACCAA CAACTTGGGGTAGGGCACCTGAACTAGTTTCAAACGGCGGCGGTTCGGCCTTTT CAGCTTTTTCGCATTTGCCATTTTCCCGCGG
25		
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003711
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG4275 - mor transcription factor involved in chromatin remodelling
30		
	<b>Human homologue of Complete gene candidate</b>	CG4275- 4507081 [ref]NP_003066.1[pSMARCC 2] SWI/SNF related, matrix associated, actin dependent 35 regulator of chromatin, subfamily c, member 2(aa)
	<b>Putative function</b>	Transcription factor, regulator of chromatin
40		
	<b>Confirmation by RNAi</b>	Decrease in G1 and G2/M and increase in polyploidy

**Example 40 (Category 4)**

**Line ID** 407/8  
**Category** Meiotic defects in testis: cytokinesis defects  
**Reversion** ?  
**Map Position** 64B1-2

**Rescue ID** A9E

**Rescue Sequence**

10 GACTCACCCCTTTCACGCATTTTCATTGGAACGTTTGTTCGTTTATGCACACGC  
 GTGTTGACACTTTTCATGAAACGCAGTGCGTGAAAAGTGCATCGCATAAACGC  
 AATAAATGTTTGATGGATGCGTTCTGATGGCTTGAAGTCGCCTATTTGGCCGA  
 TTTTCGCACGTCCACTCCCGACGGCAACAGAGTCCTGACTGAATCCCGGAGCG  
 GAAGGAGTGTGGATAGCCAGGACTGCCAAAGGACACTGCGCACTTTTACTTTT  
 15 TCGAAAGCGAAAGCGAAAGTGGTGGGGCCCAGGCCAAAACAANCCCTTGAGT  
 TGAAATTGGAAAAAAACCGGGACAGGGATGGGAGCCCAGCTCCAACAAACG  
 GTTCCGGATTTCCTTGGGAAAGCCACGCCCTGCGCCTGGAAAAGGAATGCCCTC  
 CACCTCATTTGTCTCCGTTTTTGCCTATCTCTCCCCCAAATTTCCGTTAAATG  
 AAAAACAACTTTGGGTTTTTGGTTTTTAACAATTTCTCCCCATTTGGTTTTNGGG  
 20 TTTCCCTTTCCATTTTTTGAATTGGTTTTTAATTAAT

**Genomic hit, Accession No.** AC005814 64A6-64B6

**Associated ORF**

25 Genscan ORF1 predicted sequences >22:57:22|GENSCAN\_predicted\_peptide\_2|524\_aa  
 MGRRKDKPRVIPEQDARICRAICLCQLTMVLSCVSIVYLSVAIYSPSLKAFKSGFEL  
 DPVMCQTVDRQMPNCPWASCGEWCLTKTSGFCPQIHSIVRRNGTDIQLNNCTR  
 VTNTSCAMIDLSRLNKFNCNNGTACNNIRGVFNCSNGHCKNMSEFFLCHHKADG  
 LTVNSQKDNTKLNNGFECHGVHCTKIKKPFSCDRYCSKITTTNVNTLIMHEDNLIA  
 30 ADCENAVAFNQARGSEHGVRIEPFEFWKEDDGNLLTNCA TVTRESNRRITATDCI  
 NGTLLEHDTLPAPFMNFTQFWAIYENSTRSVDPEQRYLPNQANLTIYSWKLFINL  
 EGCVNTLRGECKDFVARYGNDGDNNTAQSR YQCYYNKDSNVEFVVARYDLDK  
 VYRELLVSLIVPIVLFVISSISLCITKSVKVGDDAKMRCVCAGDDSDNDGPFPGPL  
 ANKQQDQMYD TDDDVVDLEHQA VDGQELSDHGLPLDNQELIGSTKSLIPSPVGE  
 35 SGTSDQIFDQDEKATTCDVPEKPLVIL

>22:57:22|GENSCAN\_predicted\_CDS\_2|1575\_bp

atggggcggcgaaggacaaacgcgggtgattcccgaacaggatgcgcgcacatctgcgcgccatctgcctgtgccagctgac  
 catgggtgctgtctgcgtgtccatcgtctacctaagcgtggccatctactgccctccctaaggccttcaagtcggcttcgagct  
 40 ggatcccgtcatgtgccagacgtggatgccagatgcccaacaactgccctgggcacatctgcggcgagtggtgcctgacca  
 agaccagtggcttttccccagatccactcaatagtcgctgcgaacggcaccgataccagctgaacaactgcaccagagtcac  
 caacacatcgtgcgccatgattgacctgagtcggctgaacaagttcaattgcaacaacggcaccgcctgcaacaatatcagaggc  
 gtcttcaactgtccaatggacactgcaagaatatgtcggagtctctgtgtcaccacaaagccgatggacttacgtcaattcgc  
 agaaggataacaccaagctgaatggattcttcgagtgctacggggtgactgcaccaagatcaagaagcccttcagctgcgatgc  
 45 ctactgttccaagataacaactaccaatgtgaacaccttattatgcacgaggataatctattgccgccgattgtgagaacgcagtg  
 gcttcaaccaagcccaggatccgagcaggtgtgcgtatcgaacctttgagtttggaaaggatgatggcaacctgctga

143

ccaactgcgccacagtcacaagagagtcggacaatcgcatcactgccacggactgcataaatggaaccctcctggaacatgaca  
 ccttgcccgcctccctcatgaacttcacccagtttggccatctatgagaacagcaccaggctcggatcccagcagagggtac  
 ctgcccacacaggccaacctgaccatctacagctggaagaaactgtcatcaacctggagggtcgtgtaacacactgcgtggg  
 5 gactgcaaggactttgtggctcgtatggcaacgatggcgataacaacaccgccagtcacgctaccagtgtactataacaagg  
 actcgaatgtggagttgtggtgcacgtacgattggacaaggttacaggagcttctagtctcgtgattgtgccattgtgctc  
 ttgtgatctcatctatcgttatgtatcatcaccaaatccgtcaagtggtgacgatgccaagatgcgtgtgtgtgcccggcga  
 tgattcagataatgatggccccttggcccaggactagcaacaagcagcaggatcagatgtacgatacagacgacgatgtagt  
 gacctggagcaccaagcgggtggatggtaagaactatcgaccacggacttccgtggacaaccaagagctaactggtagcac  
 caagtcgttgataccaatcagtcgccgtcggaatccggaactagtgtatcaaatcttgaccaggatcaggagaaagcaactacgt  
 10 gcgatgttcccagagaaaccactagtcatactataa

(corresponds to CG15003)

- Annotated *Drosophila* genome genomic segment AE003480  
 15 Annotated *Drosophila* genome Complete gene candidate CG15003- novel unknown  
 Human homologue of Complete gene candidate none  
 20 Putative function No homologies to suggest function  
 Confirmation by RNAi Only wild type profiles observed

**Example 41 (Category 4)**

**Line ID** 422/28  
**Category** Meiotic defects in testis: segregation defects, multipolar spindles  
 5 (Mul-02/22)  
**Reversion** NR  
**Map Position** 68E  
  
**Rescue ID** 2I4E  
 10 **Rescue Sequence**  
 TCGTGGACCCTCAAAGNAACGGATTTCTCCAGTTTCTTCAAAGGGTTAATAAA  
 CTTTTCGCACGTTTCGCATTTTTATGCTCAATCCGGTTACAAAATGCTGATAAA  
 ACCACTTGAACACACGTTTCCGTACTGATAAGGGCCTTTCTTCTTATCTGACC  
 TCTGGAATCCGCGGAATTAATTCTTGAAGACGAAAGGGCCTCGTGATACGCC  
 15 TATTTTTATAGGTTAATGTCATGATAATAATGGTTTCTTAGACGTCAGGTGGCA  
 CTTTTCGGGGAAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATT  
 CAAATATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATAT  
 TGAAAAAGGAAGAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCTTT  
 TTTGCGGCATTTTGCCTTCCTGTTTTTGTCTACCCAGAAACGCTGGTGAAAGTA  
 20 AAAGATGCTGAAGATCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCT  
 CAACAGCGGTAAGATCCTTGAGAGTTTTTCGCCCCGAA

**Genomic hit, Accession No.** CSC:AC014962

25 **Annotated *Drosophila* genome genomic segment** AE003543  
**Annotated *Drosophila* genome Complete gene candidate** CG5684 (putative  
 transcription factor, human  
 homolog  
 30 **Human homologue of Complete gene candidate** 1e-100 4758946  
 ref|NP\_004770.1|pPOP2|  
 POP2 (yeast homolog)  
 >gi|4106061|gb|AAD02685|  
 35 (AF053318) CCR4-associated  
 regulator of polymerase II  
 transcription

40

**Putative function** Transcription factor

**Example 42 (Category 4)**

	<b>Line ID</b>	422/5
	<b>Category</b>	Meiotic defects in testis: segregation defects, abnormal spindles (Ab-04/26)
5	<b>Reversion</b>	?
	<b>Map Position</b>	82D
	<b>Rescue ID</b>	B9E
10	<b>Rescue Sequence 1</b>	ATTGGCTCTTGATGGACTACAACGCTACCAAAATGGGGCTTGAGTTGAATTAC CTGTTGGAAGACACAATGCCACCCACGATCAACAATTCGGCGGTAAACAGTG CCGCCGAAAAGCGACCCAGCGGCAAACGGGAGCGCAAGTAAGTGAACAGAT CCCTAAACAGACCCAGATACTCAGACTGATGTGTACCTTGCAGATCCGAGATC 15 ATTTGCCGCGTGAAGTATGGAAACAACCTGCCGGATATACCATTTGATCTGAA GTTTCTGCAGTACCCCTTCGACAGCCACCGCTTCGTGCAGTACAACCCAACGT CGCTAGAGCGTAACTTCAAGTATGACGTGCTGACGGAACACGATTTGGGTGTC ACGGTGGGACCTGATTAACCGGGAGCTCTATCAGGCCGACTCCATGACGCTGC TGGACCCGCCGATGAAAACTGCTGGAGGAGGAGACTCTGACGCCACAGAC 20 TCTGTGCGTTCGCGCCAGCATTCGAGGACGGTGTCTATGGTTGCGAAATCCGA GT
	<b>Rescue ID</b>	B9B
	<b>Rescue Sequence 2</b>	GGCCAAATCTAGAAATCCTCAAATCTGCGCTTGGCAGTGTGACCGTACTTGAC 25 CGGTACGATAATACCTCCGGTAAAAAAATACTATATTTCCGGGGGACTCAAA TGCAACATCCTCATCGTATATAACACAACATCTATTTGAATTTCAATTTCCACAA CTAATATTATGGATAATGCTTTATTATCATTTTCCAAGTTAGCGATAAATCACC CCACAAGCTGAAAAATCAACGTTTAAAAACGATTGATATTTTTTTTAATACTTT 30 TTGGTTTTACTATTTGAATTTTGTATACTTTTAGATTTTACTATTTTAATTTTC GTTTCTTCTAGCTGACTAACGGGTAAAAAAGGATCCGTCGACCTGCAGATCT CTAGAAGCTTGCCTTGCTGGCGTTTTTTCATAGGCTCCGCCCCCTGACGAGC ATCACAAAAATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATA AAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCCGTGCGCTCTCCTGTTCCG 35 ACCTGCCGCTTACCGGATACCTGTCCGCTTCT
	<b>Genomic hit, Accession No. AC008189</b>	
	<b>Associated ORF</b>	
	Genscan ORF1 predicted sequences >15:53:24 GENSCAN_predicted_peptide_3 211_aa 40 MRNANESSGKPKSKFVSNEFHALFSTICSIADSPAVSREKLKIDLAARKIPSASAPK GDSPLERFSRDLFTYLRVCRWGRFSAALFTAELLIVGGIVSSNRTSESSETGNPLA NEPDPLYMKLVDPMVAGESPKRMIKDQKDVGLKSTSSSEELRKLPKTRGRQKRFI RNPNYVKANEFYDKMLSSEYVSKRYKDLPPHPGFGADQPPA	
	45 >15:53:24 GENSCAN_predicted_CDS_3 636_bp atgcgcaacgcaaatgaatcgagcggtaaacaaaatcgaaattgtaagcaacgaattccacgcattgtttcaacaattgttcaa	

146

5 ttgccgattccccggctgtctctcagaaaaattgaaaatcgatttagctgctcggaaaatccttcggcatcagccccaaagg  
gattctccacfcgagcgtctttcgcggatctgttcacttacttgcgtccggttgcgctggggctgcttttcgcggcactgttacc  
gccgaattgtgatcgtgggtggcatgtgtcttccaacagaacgtcagagtcttctgaaactggaaccacttgcacacgagccc  
gatccattatatagaaactgttggtatccatggtgacaggagaatcacctaaaaggatgattaaggatcagaagaatgtaggcctt  
aaatcaactagcagtgcgaagagctccgaaaattgccaaaaacgcgaggtcgacagaagagattccttgcgaatcaaaactat  
gtgaaagctaacgaattctatgataagatgtaagcagtgaaatcgtaagtaagcgggtataaggatcttcgcgcctcatccggga  
tttgagcgggatcaaccgccagcatga

Corresponds to CG2503

10

Annotated *Drosophila* genome genomic segment AE003605  
Annotated *Drosophila* genome Complete gene candidate CG2503 - novel possibly  
RNA binding

15

**Human homologue of Complete gene candidate** 3287674 AC005239  
(AC005239)  
F23149 1(aa)

Putative function	Possible RNA binding protein
Protein involved in the regulation of transcription	Protein involved in the regulation of transcription
Protein involved in the regulation of translation	Protein involved in the regulation of translation
Protein involved in the regulation of cell growth	Protein involved in the regulation of cell growth
Protein involved in the regulation of cell death	Protein involved in the regulation of cell death
Protein involved in the regulation of cell differentiation	Protein involved in the regulation of cell differentiation
Protein involved in the regulation of cell migration	Protein involved in the regulation of cell migration
Protein involved in the regulation of cell adhesion	Protein involved in the regulation of cell adhesion
Protein involved in the regulation of cell signaling	Protein involved in the regulation of cell signaling
Protein involved in the regulation of cell metabolism	Protein involved in the regulation of cell metabolism
Protein involved in the regulation of cell homeostasis	Protein involved in the regulation of cell homeostasis
Protein involved in the regulation of cell development	Protein involved in the regulation of cell development
Protein involved in the regulation of cell differentiation	Protein involved in the regulation of cell differentiation
Protein involved in the regulation of cell migration	Protein involved in the regulation of cell migration
Protein involved in the regulation of cell adhesion	Protein involved in the regulation of cell adhesion
Protein involved in the regulation of cell signaling	Protein involved in the regulation of cell signaling
Protein involved in the regulation of cell metabolism	Protein involved in the regulation of cell metabolism
Protein involved in the regulation of cell homeostasis	Protein involved in the regulation of cell homeostasis
Protein involved in the regulation of cell development	Protein involved in the regulation of cell development

20

<b>Confirmation by RNAi</b>	Almost no G1 and broadened G2/M indicating arrest in G2/M
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**Example 43 (Category 4)**

	<b>Line ID</b>	423/14
5	<b>Category</b>	Meiotic defects in testis: cytokinesis defects, abnormal spindles (Ab-16/13)
	<b>Reversion</b>	R
	<b>Map Position</b>	67B1-10
	<b>Rescue ID</b>	E9E
10	<b>Rescue Sequence</b>	
		GTTTGGCGTAAAAGCTTCGGCTGTGTTTGGTGCCCAAATTTTCCACTGCTTCT
		CTTTTGTGTATCTCTTATATCTTGTGCTTTTTTGTGTGTATGTTTTCTCGTTTC
		TTTTTGCACACGCGCTTCGCGTTGCGGGCCAGCTGTTTTGTGTTGATAAGTGGT
15		TACGGTTTGTGTGTGCCAGCGGGTTTCTTAGTCGAACTGCTCGCGATGACTG
		ATTTTTCAAAAGTGAAGTCAAAAACAGTCGATCGCCCTTTAAGAAAACCCGCT
		CAACGCACACAAAAGCGGTTTCTCTCTTTTTGTGCTTCTCTTTTCACACTGA
		CCACACGGAACGAAAAAATGATTACCGACCACACGGAAGAAAAATTTATGT
		CCAGACGAACTATTTTTGTCCAAGTCTGATTTGCATAACAATTTAAGCCA
20		CAAGAACTAGATTAATAATTTACATTTAAATACATTATCAAATCCGAAATAT
		CAATAATTGTAATTTATCCTTACAAAATGTTA
	<b>Genomic hit, Accession No.</b>	CSC:AC020214
	<b>Drosophila EST</b>	several including LP12306 (AI297868)
25	<b>Annotated Drosophila genome genomic segment</b>	AE003552
	<b>Annotated Drosophila genome Complete gene candidate</b>	CG3967 - novel
	<b>Human homologue of Complete gene candidate</b>	none
30	<b>Putative function</b>	No homologies to indicate function
	<b>Confirmation by RNAi</b>	Only wild type profiles observed



**Example 44 (Category 4)**

<b>Line ID</b>	427/5
<b>Category</b>	Mitotic defects in brain: anaphase defects. Meiotic defects in testis: segregation defects, abnormal spindles (mitotic : Overcondensation, lagging chromosomes/less aligned metaphase with bipolar spindles, Meiotic: Ab-06/20 )
5	
<b>Reversion</b>	?
<b>Map Position</b>	67B1-5
10	
<b>Rescue ID</b>	H4E
<b>Rescue Sequence</b>	GTACAGCCTGAAGTGATCGTTGTTGTTTGAATCGGTGCTATCGGCGGTTGCGC TTTGTGGGCATCTTTATCCAATTTGCTATGCGCGCTTGCCTTAAATTTTGAAC TGTATTCCAAGGTTGCTTTGGCGGCTATCGATAGTATCGGCATGGTTACATTT 15 TAGTTTTATAACAAGAATTTTACAGGTATTTTGATTATCTGAGCTTAGTTTTAA GCAANAATATTATTGTTAAAAATTTAAAAAGTAAACAAGCTATTTTAACAAGC ATTTAAACAAATAGTATTAATAATAAAAAATATATCGATATGTGTTGCAAAT GTTCGTTCCCTTAGTATTCTCTCATATTTATTTCAAATAAACTGTATAAAATAT CTGAAAAAGCGAACATATTTATTTAATTTTCATCGCAGATATCGATATCACAGC 20 GCTGCTATCGATGGTGTGTCTGTCTGCGAGTGCCTATCGCTTACCCTGCCATCGCT AACAAAAA

**Genomic hit, Accession No.** CSC:AC020120

25	<b>Associated ORF</b>
	Genscan: ORF2 predicted sequences >22:06:07 GENSCAN_predicted_peptide_7 464_aa MPSEQHTNIKVAVRVRPYNVRELEQKQRSIIKVMDSALLFDPDEEDDEFFQGA KQPYRDITKRMNKKLTMEFDRVFDIDNSNQDLFEECTAPLVDAVLNGYNCSVFV YGATGAGKTFTMLGSEAHPLTYLTMQDLFDKIQAQSDVRKFDVGVSYLEVYNE 30 HVMNLLTKSGPLKLREDNNGVVVSGLCPTPIYSAEELLRMLMLGNSHRTQHPTD ANAESSRSHAIFQVHIRITERKTDTKRTVKLSMIDLAGSERAASKGIGVRFKEGAS INKSLALGNCINKLADGLKHIPYRDSNLTRILKDSLGGNCRTLMVANVSMSSLT EDTYNTLKYASRAKKIRTTLKQNVLSKMPTEFYVKKIDEVVAENERLKERNKA LEAKATQLERAGNSGFDPLELKTWYSKIDAVYAAARQLQEHVLMRSKIKNINY 35 RQTLKKELEEFRKLKMCVDQRCQESF

	>22:06:07 GENSCAN_predicted_CDS_7 1395_bp atgccttcggaacagcatcacgaataaaaagtgccggttcgctacggccgtataatgtccgtgaattggagcaaaaacagcgga gtattatacaaggatcatggtcgttcgacatccgacgaggaggacgatgagttcttcttcagggcgccaagcaac 40 cgtaccgcgacatcaccaagcggatgaacaaaagttgacctggaattcgacagggtattcgatatagacaattccaaccagga tctgttcgaggagtgacgcgcgctggtcgacgcggtgtaaatggatacaactgctcgggtattgtatatggagccactggcg ccggaaaaacattcacatgctgggcagcgaggctcaccgggtctgacctatctaccatgcaagatctctcgataagatccaa gcgcagagcgacgtgcaagttcgatgtgggggtatctatctagaggtgtacaacgaacatgtgatgaatctgtaactaaatc gggccctttaaaacttcgcgaggacaacaatggcgtggtggtcagtggtctttgtctcacgccatctacagtgccgaggagctgc 45 taagaatgctgatgctgggaactctcatcgactcagcaccacacagatgccaatgcagagagttccaggtcacatgccatcttc caggtgcacattagatcacggagcgaagaccgacacaaaagaacggtcaactatccatgatcgtcggcgagtgagtgga gagggcgccagtagcgaaggcattggagtgcgattcaaggaaggcgccagcatcaacaaaagtccttagctttgggaaattg
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149

cataaacaagctagccgacggcttaaagcacatcccgtaccgagctcgaacctgacacgcacccctgaaggactcgttggcgagg  
 aaattgtcgacattgatgggtggccaatgtctcgtatgagctcactgacctatgaagatacctacaacacccttaagtacgctagccg  
 agctaagaagatacgacgactctgaaacagaatgtcctcaagtccaagatgccaaccgagttctatgtgaagaagatcgacgag  
 gtggtagccgagaacgagcgaactcaaagagcgcaacaaggcgctggaggccaaggccactcagttggagcgcgcccggcaat  
 5 agtggattcgatccgctggagcttaagacgtggtacagcaagatagacgctgtatatgcggccgcccgagcttcaggagcac  
 gtccttggtatgcgtagcaagatcaagaacatcaactaccggcagacactgaaaaaagaactggaggagttcaggaagctgatgt  
 gtgtcgaccagcgagtggtgccaggagagttttaa

**Drosophila Gene Hit** TBLASTN with ORF2: kinesin like protein 67a (U89264)  
 10 **Human Homologue** TBLASTN with ORF2: kinesin family member protein KIF3A  
 (AF041853)  
**Drosophila EST** GH22018 (AI402731)

**Annotated Drosophila genome genomic segment** AE003552  
 15 **Annotated Drosophila genome Complete gene candidate** CG10923 Klp67a -  
 motor protein

**Human homologue of Complete gene candidate** 2e-58 4758646 kinesin family  
 protein 3B  
 20 >gi|3913958|sp|O15066|KF3B  
 \_HUMAN KINESIN-LIKE  
 PROTEIN KIF3B and also  
 predicted peptide  
 ENSP00000166696  
 25 Gene:ENSG00000073652  
 Clone:AC015936  
 Contig:AC015936.00023  
 6.70E-91 (predicted kinesin?:  
 ENST00000166696)

**Putative function** motor protein involved in cytoskeleton organization and  
 biogenesis

35 **Confirmation by RNAi** Almost no G1 and broadened G2/M indicating arrest in  
 G2/M

**Example 45 (Category 4)**

	<b>Line ID</b>	442/3
	<b>Category</b>	Meiotic defects in testis: segregation defects.
5	<b>Reversion</b>	?
	<b>Map Position</b>	70D4-7
	<b>Rescue ID</b>	H7E
	<b>Rescue Sequence</b>	
10	CGCAAGACTGTCTTCGATAGCAGAAGCGTTATTTGGAACATATCGTTTATCG	
	AAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA	
	ACCATTTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT	
	AAAATATAAACTACGAGGATCAAATATACATACATATCCCAATATGTTAGCG	
	AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA	
15	TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGACATTTCAT	
	ATTTAAATATATTTTAAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT	
	GTAAGTGTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCATC	
	GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA	
20	<b>Genomic hit, Accession No.</b> CSC:AC017664	
	<b><i>Drosophila</i> EST</b>	CK02287 (AA141680)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003536
25	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG6650 - novel transacylase like
	<b>Human homologue of Complete gene candidate</b>	none
30	<b>Putative function</b>	Transacylase
	<b>Confirmation by RNAi</b>	Marked increase in G1 indicating arrest in G1
35		

	<b>Line ID</b>	473/22
	<b>Category</b>	Meiotic defects in testis: no division (no meiosis)
	<b>Reversion</b>	R
5	<b>Map Position</b>	70A1-5
	<b>Rescue ID</b>	2B7E
	<b>Rescue Sequence 1</b>	
10	CGCAAGACTGTCTTCGATAGCAGAAGGCGTTATTTTCGGAACATATCGTTTTAT CGAAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTC AAACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAA TAAAAATATAAACTACGAGGATCAAATATACATACATATCCCAATATGTTAG CGAAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTT TATGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTT 15 CAATTTAAATATATTTTAAATATATTCAAATATAGTATAGCAGTATAGCATTCAA ATGTAAGTGTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTCA TCGCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATAAGAA AGTTGGCGTAGCCGGAAGGCGGATTGTCACATACAAAATAGTTTGGAAAGCC CAAACGTGAG	
20		
	<b>Genomic hit, Accession No.</b>	CSC:AC017664
	<b>Drosophila EST</b>	LD47104 (AI515336), SD03663 (AI532240)
	For other results see line 442/3	
25		
	<b>Line ID</b>	670/6
	<b>Category</b>	Meiotic defects in testis: segregation defects, abnormal spindles (Ab-12/48)
30	<b>Reversion</b>	?
	<b>Map Position</b>	70C
	<b>Rescue ID</b>	H7E
	<b>Rescue Sequence</b>	
35	CGCAAGACTGTCTTCGATAGCAGAAGGCGTTATTTTCGGAACATATCGTTTATCG AAACTACAGTTGCTCAATACTGAACTGTCCAGCTTCGAGTAGCTGTGGCTCAA ACCATTGTTGTCATCGATAAGCAATTGCAATTTTATTTGTTTGCTTAAAAAATT AAAATATAAACTACGAGGATCAAATATACATACATATCCCAATATGTTAGCG AAAAAACATTTCTGCTCAAAAAAAGATGTTTAAATACAATGTAAGCTGTTCTA 40 TGCATTGAACAAATTAACACATTGAGAGGTCGCTCTTATAAGTGCACATTTCA ATTTAAATATATTTTAAATATATTCAAATATAGTATAGCAGTATAGCATTCAAAT GTAAGTGTGGTTGGACTATCGCTGTAGTCCAAGAACTGCAGATAGTGTGCATC GCTAGCTTTGAAGCATCTCAAAGGAAAAAGGGCGATAATTCTGATTA	
45		
	<b>Genomic hit, Accession No.</b>	CSC:AC017664
	<b>Drosophila EST</b>	CK02287 (AA141680)
	For other results see line 442/3	

**Example 46 (Category 4)**

	<b>Line ID</b>	460/20
5	<b>Category</b>	Meiotic defects in testis: segregation defects, multipolar spindles (mitotic: High polyploids, no diploids, higher mitotic index Meiotic: Mul-02/59)
	<b>Reversion</b>	NR
	<b>Map Position</b>	78A1-4
10	<b>Rescue ID</b>	2B8E
	<b>Rescue Sequence</b>	
	AGCTGGTCCAATTGGAAACGTTAGCTGCTCCAATGGGAGCAGCTGGCGCTCTC	
	TCTTCGATCGCGCTCGCTCTCATCCTCTCTTTAGCTTGTGCCACAGTAGCTG	
	CCGAAGGCAATTTTCATGTGCTCGTGTGTCGACCCCCACTCAGCCCACTTCTG	
15	ATCGGAATCGGGGATTCGGAATCGTGTAAGGCAGCCTTTGAAGGTCCCTTTTC	
	CAGGTGGCGGCCGTATCCTTAAAGTAAACATAGTTCAACTGACTTGGCAGCGC	
	TCCAAATGCGGTGACTTCTTGGCTATGTCATATATACCCCCACTCCCCTCCTGA	
	CTACCCTGCCACGCCCCACGCCCCACGTCGGCGACGACAATTCCATTAAAAG	
	TTGTACGTTGTCACTTTGCGTTAACTTATCTGTGGAGCATGTTGTGCGATCGCA	
20	TTTTTATTGTCGCCATTGTCTCTCGCTCTCTCCATCGCTCTTTCGCCTGGCTTCC	
	CTACCCTGCCACACAGGGAAGCCTACACACTCTTAAATCATGCACTTGGAAC	
	AAAAAGTGCAAGCATTAACCTTTATTTAAACATTCAAGAGCCGCTTCTCTATT	
	TACCATTGAAAATTTAATTTAAAATAGAAGAGGCCTTTTCAGAATAATATAAT	
	ACCTTTAAG	
25		
	<b>Genomic hit, Accession No.</b> CSC:AC020460	
30		
35		
40		

**Example 47 (Category 4)**

**Line ID** 477/16  
**Category** Meiotic defects in testis: segregation defect.  
5 **Reversion** NR?  
**Map Position** 90C5-10

**Rescue ID** C3E

**Rescue Sequence 1**

10 CTGTGGACGGTCGTCGAATGCGTGAATATTCTTCTATGTGTAAGTGGTGTGCGT  
GTATGTAGATTTCTGGTTAAGAAAAGCCCCAAAAACCAAAGCGCCCCGCAAA  
ATATATATTGAGTCTTCTTGGCCCAACAACAAATCTGCCGCCGGACTTTCGCC  
GGAGGGCGAGTGAAAAATTCAGTTTCTCTCCTCTCGACGATGCACTTTGGAGG  
CTGTGTGAGTGTGTGTGCGAGTGAGTGCGTGTGTGTATACATATGCAAATGAT  
15 TGGATGTCGAATCCTTGCATCATCATCTTCATAAAACACTTGGCGAAAAAC  
CGCAGGAAAACGCAAGCAGCCGAACAAAAAAGAGAGCCTCTCAAGACAAC  
GGCAGCGGCCAAAAGTGAACGCGCAACAAACGCGGCCAAGCAGGCGCGGCA  
ATTATTTATAAATCTTAAGCCGTTAGCCCCCTCTCTCTCCCACTCACGAAAAG  
AAAATAAGTTAAACCAATTGGTGAAGATGATGCCCC

20

**Rescue ID** C3P

**Rescue Sequence 2**

GTCCACAGACTGGCTATATATACTAAAAACGAACTCGCGTGAGAAGACAGGG  
ACAGGGCAGCAAACCTCGGTATACGAACGGAACGAAATGAAACGATTCAAGTA  
25 GTAGTGTATGCAAGTCTTGTCTGTCTGCGCCTGGCGTTCTTTTCTTCTTTTTT  
TCGATGGTTTTTCGCCAGGCTGGGCGCTGCCAAAACGCTGATACGGCGGCCAC  
AATCACACGCGGCTAATCGCCAGTTGGGCCCTGCACAGGCTGCACATACTTTT  
CACTATTAATGCGCTGTATTTCACTTATTTTTCGAACAAATTCGCAGCATGACG  
AAGAAGCGAGCCTGTACAAGATTAGAGCGGGTAGCACGCACGATAGTATCGA  
30 TACGTACGAGTATTTGGCACTGCGATACATTATCGGTGCTCGTTTCGATAGCCC  
CCGATAGCTCTAGCACGAAATTTTATCGCTTTATCCATATTTTATACTATTTTT  
ATTTATTGGACTTCAATGAATATTTAATTTACGTCTGGGTCGCTTTTTAAATAT  
ATATGGTAATCAATAGCTGGCGAATTAGCGATATTTGAGTGTGACGCAAAAAT  
GAGTTGCATCGATATCGATTTCTCGCTACTCTGGGACGCCATCTTTATTGCGG

35

**Genomic hit, Accession No.** AC007810

**Associated ORF**

Genscan ORF1 predicted sequences >17:48:58|GENSCAN\_predicted\_peptide\_2|349\_aa  
40 MSRLFILLLLIVTQLSELQAAAFSVRQNRFDVDPDLQTPAPLATSTESSKKPEKAT  
SGLLKKCLPCSDGIRCVPQIQCPAHVRMESHEKPQICDLPAGKFGYCCETGQNHT  
APKPETSPKERRSGFPTILSPAVLDEARRNFEHLMHGVAQIPVRRGFDPFAHGLVF  
HSTAKDDLHNFAISNSAIEQVMTTQLFGKKEQVPVEDFITNNVPIKFTETPLAHHC  
QPPPVCGNIRSVYRSMGTCNNPEPQRSWGAAGQPMERMLPPAYEDVPSASPA  
45 AICSYIYGIASRLAPVSVVNCCTFAWQLDWTTGMASGECVCVECMPAEWRLGQC  
PLLHEASSEMSRLLAKS

>17:48:58|GENSCAN\_predicted\_CDS\_2|1050\_bp  
atgagtcgcattttattttattgttctactattgtgacgcaactgagcgagttgcaggcggcgacattttctgtcgccaaaatcgtt  
ttgatgaagtctctgatttcgagactcctgcacctctggccacttccactgaatcttctaagaaacccgaaaaagctaccagtggtct  
5 gctgaaaaaatgccttccctgcagcgatggtataagatcgctgccccaaatccagtgtcccgccacgttcgcatgaaagccat  
gaaaagccccaaatttgcgatctccggctggaaaattcggctactgctgcgagactggacagaatcacactgtctccaagccg  
gagaccttcccaaggagcgtcgatccggatttccaccattctgtcaccgcagtttggatgaggcgcgtcgcaatttcgagca  
cttgatgatggagttgcgagattccggctgcgcgttggttccagattttgccatggcctggttttccactgcacggccaaggat  
gaccttcacaacttcgcatatcgaaacagtgccattgaacaagtatgaccaccagttgtttgggaagaaggagcaggtgccg  
10 tagaagatttcacccaacaatgtgcccataaagttcactgagactccgctggcacaccattgccaaccgccccagtttgcggc  
aataatcggtctgtttatcgagcatggacggcacttgcaataatcgaaccacagagatctctgtgggtgctgtgtgtcaaccg  
atggagcgcgatgctgcccccgccatgaagatgtccgtcagcttctctgctgctatagtgttatatctatggcatcgcatctcg  
cttggcgccgtgttctgtgttcaattgttgacatttgcattggaattggattggaccacttgaatggcgagcggggagtgtgtgtg  
gtggaatgtatgccggcgagtgggcgtttggccaatgccgttgcttcatgaggcgtcgagtgaaatgagccgcctcttggcta  
15 aaagctag

	<b><i>Drosophila</i> Gene Hit</b>	rescue sequence: eyelid/osa (AF053091)
	<b>Human Homologue</b>	BLASTX with eyelid: KIAA1235 protein (AB033061) Brain protein 120 (AB001895)
20	<b><i>Drosophila</i> EST</b>	several including LD04852 (AA201670), LD24466
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003718
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG7467 - osa DNA binding putatively involved in DNA packaging
25		
	<b>Human homologue of Complete gene candidate</b>	CG7467 - 7e-25 2588991 dbj BAA23269  (AB001895) B120 [Homo sapiens] and O14497 SWI/SNF-RELATED, MATRIX-ASSOCIATED, ACTIN-DEPENDENT REGULATOR OF CHROMATIN SUBFAMILY F MEMBER 1 3e-67
30		
35		

40 **Putative function** transcriptional regulator

**Confirmation by RNAi**      Only wild type profiles observed

**Example 48 (Category 4)**

	<b>Line ID</b>	496/4
	<b>Category</b>	Meiotic defects in testis: segregation defects, abnormal spindles (meiotic: Ab-08/42)
5	<b>Reversion</b>	NR
	<b>Map Position</b>	65E4-7
	<b>Rescue ID</b>	2C1E
10	<b>Rescue Sequence</b>	GCACGATCGCTCTCTCTTGGCTCTCTCTATCACTCTCTGGACTCTCTCTCAGCA CCTTTGCTACCGTTTCGCAGAACAGGTGTATCGGTTTTCAAGGCAACTGTGATT TTTTAACTCAACATTCTATATCGAAAACCTTGTAAGGTCGGAATTTTTCTTGAG CGCCTAAAAGTGTGCAGTGAAATCATTAAATCCACTTCCGGTTGCAAAACAGG 15 AATCACACATATGAAGTGATTAATAATCATAGAAGGTTTGACACCTTCAAATA ATAAGAAAACAAAAATTTGTAACTGTGATAATTTATTTAATTGAAATCTTAA TTTAATGGCCTACAAATCTGTTGAATATCCGTTGAATACACTTTCCAGGGTGT GTCCTAGTCGGCTCCTCTTTGTTACCCAGTTTGCTGGTCTTCTTAGCCGCACA CCAGTTTATCGCTGTTTGCCTTTGCGCTTTTCATTATATAACAAAAACAATG 20 TTATTGTTATTGCGGTGGCTGTAGATGTAAATGTAAATGTAGATGTAGAGGCT GCTTCTTGGG
	<b>Genomic hit, Accession No.</b>	CSC:AC018039
25	<b>Associated ORF</b>	Genscan ORF1 predicted sequences >19:35:36 GENSCAN_predicted_peptide_6 190_aa MVSEQFNAAEKVKSLTKRPSDDEFLQLYALFKQASVGDNDTAKPGLLDLKGKA KWEAWNKKQKGSSEAAQQEYITFVEGLVAKYDNGMHKQEPNTCQARNATRFR KSSECSLDQNTYTSSVTVIPAFHEGPKNSTASWPRIYRCYQRNQQAAANCKWANTN 30 SVCCKPHGKQSRRIIFAEFLAGHTVQILG
	>19:35:36 GENSCAN_predicted_CDS_6 573_bp	atggtttccgagcaattcaacgccgccgagaggtgaagagcctgaccaagcgtcccagtgatgacgagttcctgcagctg tacgccctgttcaagcaggccagcgttggtgacaacgacaccgccaagccgggtctcctggacctgaagggcaaggccaagtg 35 ggaggcctggaacaagcagaagggaagagcagcaggccgccagcaggagtacatcaccttggaggccgtgtggc caagtatgacaatggaatgcacaacaagaacaaacacttgccaagcacgcaatgcgactcggttcggaaaagctcggaatg ctcgtggatcagaatacgtatacgtccagtgtagcgggtatacctgcattccacgaaggtccaaagaactcgacggcaagttggc caagaatttaccggtgtatcagcgaaccaacaagcggccaactgcaagtgggcaaacacaaatagcgttcgagggaaccc cacggaaaacagagccgccgaatcatttcgcagaatttcggcggccatacggcgagattcttggttaa 40
40	<b>Drosophila Gene Hit</b>	rescue sequence: melt (S144114) P element insertion site (AF174669), TBLASTN with ORF1: diazepam binding inhibitor (DBI) (U04823 ) and melted (AF205831)
45	<b>Annotated Drosophila genome genomic segment</b>	AE003560
	<b>Annotated Drosophila genome Complete gene candidate</b>	CG8624 melt - putative signal



		transduction protein CG8631 msl-3 - acyl-CoA-
		binding
		protein/diazepam binding
5	<b>Human homologue of Complete gene candidate</b>	inhibitor
		CG8624- predicted gene
		ENSP00000065899
		Gene:ENSG00000055889
		Clone:AC015904
10		Contig:AC015904.00014
		1.70E-15 (unknown predicted
		gene 1: ENST00000065899
		and AK022666 Homo sapiens
		cDNA FLJ12604 fis 2e-29
15		
		CG8631- gi5803104
		0C85AE40FDF874CD
		[ref]NP_006791.1  male-
20		specific lethal-3 (Drosophila)-
		like 1 [Homo sapiens] (1.70E-
		36) and Ensembl predicted
		peptide ENSP0000006617
		Gene:ENSG0000005302
		Clone:AC004554
25		Contig:AC004554.00001
		8.70E-19 (unknown predicted
		gene 1: ENST0000006617
30	<b>Putative function</b>	
		CG8624: putative signal transduction protein
		CG8631:acyl-CoA-binding protein/diazepam binding
		inhibitor
35	<b>Confirmation by RNAi</b>	
		CG8624: reduced G1 and G2/M Indicating fewer cycling
		cells, CG8631: Increased G1 to G2/M ratio indicating arrest
		in G1

**Example 49 (Category 4)**

	<b>Line ID</b>	523/19
5	<b>Category</b>	Female sterile. Meiotic defects in testis: cytokinesis defects, segregation defects (Mitotic: Less condensed chromosomes, nuclear bridges, Meiotic: Seg-01/02
	<b>Reversion</b>	R
	<b>Map Position</b>	75C1-4
10	<b>Rescue ID</b>	2B4E
	<b>Rescue Sequence</b>	ACTGAGAGCATATTTGTGCACCAGAGGGCTGCATAACAACATTCTCTTTGTCC ATTCGTTATACTTCGTATTCAGAATACATGTCATTTCAGTTGGTCCCGTTCTTTTT GCGTTCACTTCGTATATAATTCGGCGATCGAAATGAACTAACTGAATGTGTTCA 15 AAGAATGAATGAAGCCAATGAATTTTCAATAGTAATTCAGAGTGCTTAAATTT CTTTCATGTTGTCATTGAGTAAAATGAGTTCGGACAGCGCGAAGGTAAAGTCGAA GTTTGTGTTTTATTATGTTTATTTGTATTATTATGTACACTAGTCGGCATACTTT TGCCTGCGTCTTATACGTGTGCGTCTTATTTAACAATATTGTAAAATAAAATAT ATAAATTATTTGTTATATGCGTAGGGGCCTTTATTTTGTGTATTGATAGTCTTTT 20 GTCATAGATATCATTATTCTGACAAGATTTGAACTTTTCAAGTTATTGCCTCTC GTTATTCAATTCCTAGCTGGTCTTACGTTACGCGATATTTCTAAAATATCCTA AAATCGCACAAAACAGTCACGCCCACACTTTTGAAAAACGTGGTAATATTTT CATACTTGCATTAAGTCTGG
25	<b>Genomic hit, Accession No.</b>	AC007691
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003520
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG4306 – novel
30	<b>Human homologue of Complete gene candidate</b>	4e-25 3242764 (AC005154) similar to protein U28928 (PID:g861306) [Homo sapiens]
35	<b>Putative function</b>	No homologies to indicate function
	<b>Confirmation by RNAi</b>	Only wild type profile observed

**Example 50 (Category 4)**

	<b>Line ID</b>	666/19
	<b>Category</b>	Mitotic defects in brain: anaphase defects (weak, overcondensation, aneuploidy, lagging chromosomes, metaphase with bipolar spindle)
5		
	<b>Reversion</b>	NR
	<b>Map Position</b>	64E1-5
10	<b>Rescue ID</b>	I9E
	<b>Rescue Sequence</b>	CCCTCGTCTACGTCGAAATTCTGGATGCTTCTCGGATTTAGGGTTGTATCTCGA AAACGTTTGACTGCGAATGTCAATATCGATATGCTAACCGATAGCTGTGCGATG TTTTAAACACAGTGCACTGTTTTTAAATCGCTCCCCATTTATATATATTTGTGC 15 NTGCTTTTGGCGGTNNTTTTCTTTATATGCTTCTTATGCTTTTACGATTATTATT AGCGCTTATTTGATTGCAAAATGCCAAGGAAAGCGTGACTGTGATGGCGAAATG CGGAAAGTACTCCTTAAATCTCATATATCGCATAAAACTATCGGTTCTGGAAT GTTTCGTGTAAGTCTGCGAAGATAGAGATCGATCTATTTTGAGGATACATTTG TTAATATTATAAGGGATTCTTCTACAGGGGTCAGATTGCTTAAAAACACACAG 20 AANAATAAACAAAAATTTTCTTTGAAATATTGAAATATTTGAAATANAAAAAA CGTATTGACGAGGTAAGCATATTGAAAAAGATAGGAAGGTGATGGAGAAAAGT GCACTTATATTGGTCCACAAAGAGCTTATAATCAAAAGATCAATAGATATAAA TATCTTTATATGATATAAAATATAATACATATAATATAATATCATATACAATG GATAAATTGCAAGTGGCAAAATGAATTCCGCGGAATTAATTCTGAANCGAAA 25 GGGCCT

**Genomic hit, Accession No. CSC:AC014815****Associated ORF**

30	Genscan ORF1 predicted sequences >17:46:43 GENSCAN_predicted_peptide_1 334_aa MGKDFYKILGLERKASDDEIKKAYRKLALKYHPDKNKSPQAEERFKEIAEAYEVL SDKKKRDIFDNYGEDGLKGGQPGPDGGGQPGAYTYQFHGDPRATFAQFFGSSDP FGAFFTGGDNMFSGGQGGNTNEIFWNIGGDDMFAFNAQAPSRKRQQDPPIEHDLF VSLEEVDKGCIKKMKISRMATGSNGPYKEEKVLRITVKPGWKAGTKITFPQEGDS 35 APNKT PADIVFIIRDKPHSLFKREGIDLK YTAQISLKQALCGALVSVPTLQGSRIQV NPNHEIHKPTTTRRINGLGLPVPKEPSRRGDLIVSFDIKFPDTLAPSLQNQLSELLPN
----	--

&gt;17:46:43|GENSCAN\_predicted\_CDS\_1|1005\_bp

40	atgggcaaagacttctcaagattctgggcctcgagcgcaaggccagcgacgatgagatcaagaaggcctaccgcaaactggc actcaaataccatcccagacaagaacaagagcccacagggcggaggagcgcttcaaggagatcgccgagcgctacgaggtgctg tcggacaaaaaagcgcgacatctcgacaattacggtaggatggattgaaggcgacagccgggaccagatggcggcg gtcagccgggagcgctacacttaccagttccacggcgatccgagggccacatttcccagttcttggatcgctggatccgtttggc cgcttcttaccggcgcgataacatgttagtgcggtcaggcgccgaataccaacgagatcttctggaacattggcggcgacg atatgtttgccttaatgccaggcaccagtcgcaagcgccagcaggatccgcccacgagcatgatctgttcgtgctggag 45 gaagtggacaagggatgcatcaagaagatgaaatctcacgcatggccaccggaagcaatgggccgtacaaggaggagaag gtgctgaggatcacagtgaagccgggctggaaggccggtaccaagattaccttccccaagagggtattcgcgccaaacaa
----	--

159

gacgccagctgacatcgtcttcattcgcgacaaaccgcatcgtgttcaaacgcgaggggaatcgatctaaagtatacagccc  
 agatcagctgaagcaggccttgtcgggagcactggttagtgcccacgctgcagggcagcaggatacaggtgaatccgaacc  
 acgagatcatcaagcccaccacaacgcgcgatcaacggactgggtctgccggtgcccaaggagccatcgaggcgcggcg  
 atctgacgtctccttcgacattaagtttccgacacactggcaccagctcgcagaatcagctgtccgagctgtgccaactag

5

**Drosophila Gene Hit** rescue sequence: fasciclin I (FasI) ( M32311) TBLASTN with  
 ORF1: DnaJ homolog (DROJ1) (U34904)

**Human Homologue** TBLASTN with ORF1: DnaJ-like heat shock protein 40 (HLJ1)  
 (U40992.2)

10

**Annotated Drosophila genome genomic segment** AE003565

**Annotated Drosophila genome Complete gene candidate** CG10578 - DnaJ-1 a  
 chaperone putatively involved  
 in protein folding. Stimulates  
 activity of HSP70

15

**Human homologue of Complete gene candidate** 8e-94 1706473 P25685  
 DNJ1\_HUMAN DNAJ  
 PROTEIN HOMOLOG 1  
 (HDJ-1) (HEAT SHOCK  
 PROTEIN 40) (HSP40)

20

**Putative function** Chaperone involved in protein folding

25

**Confirmation by RNAi** Almost no G1 peak, increased G2/M indicating G2/M arrest

**Example 51 (Category 4)**

	<b>Line ID</b>	714/11
	<b>Category</b>	Meiotic defects in testis: cytokinesis defects, abnormal spindles (Ab-01/04)
5	<b>Reversion</b>	?
	<b>Map Position</b>	66A10-15
	<b>Rescue ID</b>	2A4E
10	<b>Rescue Sequence</b>	AACCAGAACGAAACTCCAATGCAGTTTCATTTTGTCTAGTTTAATCATTAAACA AAGAACTGCGCAACCGATCGCAACTAGCTCGTGGACTCTTGTTCTCCCAATAA TTGGTATGTTTTCCATTTTTCGTTAACATGGAAAATGTGTGAAAAGCTTTTCC CCCTCCAAAAGAAGCGTACTGAACTAAGCTTTCGGTGGTTAGTAATAGTAGTC 15 GTTATATCTTATTTTTCTTATTTACGTGCAGCTGCAATCATTGGCTGCGTCACTT TGGCGTCAGCTATAAACTGGTGGATCAACTCGGCGGCCTCCAAAAGCTGCGCA TCTGCTCCAGACACTTTAGCCAACGCCAGGAGATGGCCAAAACCCGCATCAA GATGACGCCGCTGCGCAAGTCCTCGTCCTCAAAGGGCATTGTGCTACCCATTA ATGCCGCTGGAGGGTTCGGTCATTGCAGGCGCCTTAGCACGAGGAGGAGGTGC 20 A
	<b>Genomic hit, Accession No.</b>	AC012390
	<b>Associated ORF</b>	25 Genscan ORF1 predicted sequences >19:47:45 GENSCAN_predicted_peptide_2 711_aa MRSHQAVGNLLLADEALPAVQSASVYVWMAEQPLSPGQSYDIKIADSPSVSS KSITDNGADVQWFAFEHSQYYQGVQQMFLSALERIDSEFLITLIKRCPYHVDLSLVQ LSEVCKMTEDFSLASELLERALLLLESSLHINFSLTSGNCRLDYRRQENRSFYIVLF KHAQYLEERACSRTAFEISKLLLSLQPDTPDLAMILPNQPDQCTGNMTQLQQAGK 30 IRKRSEKQFPIGTEPRGTDALRFTLQTLASAGRDITWNIKRLQGSRTVGAAGGYLI DKKTAVQYKITIIAHLKDPNIDQLFDSSGDGKADLHGSTPDWGCQAMMADAISR YKEGNPVFYTTWTPYWVSNELKPGKD VVWLQVPFSALPGDKNADTKLPNAGGI EGLIADEEVQVLDALCDAPCVGVSHSCRLLDGNRRGNNELRLFIPGKSQFGVADG CADKQSVMEYHAAKTGHTKFSESEEEKKALTEEEKKAQLALIEEKLKQKRIEREE 35 REKIEALQREKNRIKSGKDMTEAKRRMEELEMKKIVEQRKREKDEEKAARDRVK AQIEADKAARKAREQKELGNAEPAPSVSSTTVSSPPAGVKSPPRDYTETRIQGASA ILAAAAPYYQPPAVPQDVQPDPIGYGAFGVVCGSHISGWHCSAGHYEDGNENFE CLKTFSTSDRIGCEWRWAAATVLAATCISPNGRCGHYKRVRRRIKTNTTTT 40 >19:47:45 GENSCAN_predicted_CDS_2 2136_bp atgagatcgcatcaagccgttgcaatctgctgctggcggcagacgaagcgttaccggcggtgcagagcgcgtcggtgtatgtg gtatggatggcggacagccgcttctcaggcagagttacgacatcaaaattgccgactctccatcggtgtcctccaagtctatc acagataatggagcgggacgttcaatggttgcctttgagcatagccaatactaccaggagtgagcagaaatgttcttctgctctcg agcgcattgactcggaatttctgatcacacttatcaaacgctgccctatcatgctgactccttggttcaactcagcgaagtatgcaa 45 gatgaccgaagacttttcttggcctccgaactgctgagcgcgcccttctccttctggaatcgtcgtgcacatcaacttcagttga cgtcgggcaactgccgactggactaccggagacaggaaaaccgatccttctacatcgtgctgttcaagcacgcgcagttacgtg

161

aggaacgagcttgccgacccgacctcgagatctccaaactgctcctgagcttcagccagacacagatcctcttgccatgatt  
ctaccaaatcagccggatcaatgtaccggcaatatgacgcagctgcagcaggcgggcaaaatccgtaagcgctcagaaaagca  
gttccgatcggtactgaaccgcgcggtactgacggttgctgctcaccctgcagacactggcgtctgcccggctcgacatcacct  
ggaatataaagcgtctgcaagggtccggtgttaccggcgcgggcccagggttacctcatcgataagaaaaccgctccagtacaa  
5 aatcaccatcatcgctcatctgaagatccgaatatcgaccaactgttcgattcaagcggcgacggaaaagcggatttacacggta  
gtacccagactggggctgccaagctatgatggcgcacccatcagctgctacaaagaggggcaaccgggtgtttattacacctg  
gacggcgtactgggtgagtaacgaactgaagcggcgcaagatgtcgtctgttgaggtgcccgttctccgactgcccggcgga  
taaaaacgccgataccaaactgccgaatgccggtggcatcgaaagcctcatcgccgatgaagaagtcaggctcctgatccct  
ttgtgatgcgccgtgtgttggtgtctccactggtccgactccttgatggcaatcgccgaggggaataatgaactgcccgtcttatt  
10 cccggcaatccagtttgagtagctgatggatgtgcagacaagcagagtgttatggagtaccatgccgcaaaaccgggtcac  
accaaatctccgaatggaggaggaaaagaaggcgtcaccaggaggagagaagaaggcccagctggccctcatcgaggag  
aagctcaagcagaacgcacgaacgcgaggagcgcgagaaaatcgaagccctgcagcgggaaaagaatcgcatcaagtcc  
ggcaaggacatgaccgagcccaagcggcgcatggaggagtggagatgaagaagatcgttgagcagcgcaagcgcgaaaa  
ggacgaggagaaaggcgcccgcatcggttaagggtcaattgaggcggacaaggcagcacgcaaggctagagaacaaa  
15 aggaattgggaacgcagagccagctccatcgtagctccaccacagttcgtcaccaccggccggtgtgaaatctccggcg  
gagactacaccgaaaccgcatccaggcgccagcgcaatcttgccgcagcggctccctactatcaaccgcccgtgttccc  
caggatgttcagccgcatcgtctatcggtatggagcattcgagttgtctgcggttcccatcagcggctggcattgttctg  
gggcattatgaagatggaatgaaaattcgagtgcccaagacatttgcacttctgaccgcatggctgcgaatggagatggcg  
gcagcaactgttcttccgcaacctgcattagcccgaacggccgttgccggcattataaacgcgtacgtcgcattaaaacaaa  
20 cataacaactacgtga

- Drosophila Gene Hit** rescue sequence and BLASTX with EST: BIP1 (Y14998),  
BLASTX with genomic sequence matches BIP.
- Human Homologue** BLASTX with BIP1: alanine:glyoxylate aminotransferase  
25 (X53414) ?
- Drosophila EST** GM04749 (AA695904), GM13608 (AA803601)
- Annotated Drosophila genome genomic segment** AE003556
- 30 **Annotated Drosophila genome Complete gene candidate** CG7574 - bip1 unknown  
function
- CG13681 – unknown
- Human homologue of Complete gene candidate** none
- 35 **Putative function** no homologies to indicate functions, Drosophila Bip1 interacts with  
transcriptional activator Bric-a-brac which is required for ovariole  
formation
- 40 **Confirmation by RNAi** Both show reduction in G1 and G2/M indicating fewer  
cycling cells

**Example 52 (Category 4)**

	<b>Line ID</b>	763/4
	<b>Category</b>	Meiotic defects in testis: segregation defects (overcondensation, fewer anaphases)
5	<b>Reversion</b>	R
	<b>Map Position</b>	90F
	<b>Rescue ID</b>	2F5E-1
10	<b>Rescue Sequence</b>	CGGCAATGTCTGCGCCCCCAATCTGAACTTGCCCTCGCCCTCTCCGCCCCCTGATC TCATCTCCTCTTCAAACCCCTGCTCCCCCTTTTCTGCACACATTAACGTCAGCCT TTAAGTGTGCTTTCTCAGGTGCTGCCCCCTGCGCCCACCATCCCCCGCTCCATG CTCTTTCCATCTTGCGCTCTCTGCGTTCTATCTACATTTTTTTTCGAGGTCGCGCG 15 CTGCTTTTTCCGTTGATGTTTCGTTCTCGTCAATGTCGCAATATGCGCAAAAGGC AGACAAAAAATGAGTGGAAAAAGTACATACATACCGGTGATTGATGGG CGGTGGGTGGCGGTGGTGTAGGNGTGGTTTG
	<b>Genomic hit, Accession No.</b>	AC006495
20	<b>Associated ORF</b>	Genscan ORF1 predicted sequences >22:47:02 GENSCAN_predicted_peptide_3 283_aa MTERENNVYKAKLAEQAERYDEMVEAMKKVASMDVELTVEERNLLSVAYKNVI GARRASWRIITSIEQKEENKGAEKLEMIKTYRGQVEKELRDICSDILNVLEKHLIP 25 CATSGESKVFYYKMKGDYHRYLAEFATGSDRKDAAENSLIAYKAASDIAMNDLP PTHPIRLGLALNFSVFYYEILNSPDRACRLAKAAFDDAIAELDTLSEESYKDSLIM QLLRDNLTLWTSDMQAEEIPIKLPDRQSKTTLIFSPRSQVNPKILHKNTTIIGRVIC SVFA
30	>22:47:02 GENSCAN_predicted_CDS_3 852_bp	atgactgagcgcgagaacaatgtgtacaaggcaagctggccgaacaggccgagcgtacgacgaaatggaggccatga agaaggctgcctccatggacgtagagctgaccgtcgaggagcgaaatctgctgtcgtggcgtaagaatgtgattggagcac gccgtgcctcgtggcgcacatcacctgatcgaacagaaggaggagaacaagggggccgaggagaaattggagatgatcaa aacctaccgcgacaggtggagaaggagctgcgcgacatctgctcgatatactgaacgtgctcgagaagcatctcattccatg 35 cgccacatccggcgaaagcaagtaattactataagatgaaggcgactaccatcgctacctggccgaattgccaccggctcc gaccgcaaggatcgggcagagaactcgtgattgcctacaaggcggccagcgatattgccatgaacgatctgccaccaacaca ccccatccgtttggccttgccattgaactctcgtgttctactatgagattctcaactcgccggaccgcgttgccgcttggcgaaa gccgtttcgtgatgccattgcgagttggatactgagcgaagagagctacaaaactcgacactcatcatgcagctgtcgc gcgacaacctcacattatggacgtccgatatgcaggcagaagagattccgattccaaaactcccgacagacagtcctcaaaacca 40 cattgatttttagccccgaagtcaagtaaacccaaagattctccacaagaacaacaccatcatcggcagagttatctgtagcgtgtt tgcgtga
	<b>Drosophila Gene Hit</b>	rescue sequence: 14-3-3 epsilon isoform gene (U84898) TBLASTN with ORF1: 14-3-3 .
45	<b>Human Homologue</b>	TBLASTN with ORF1 and BLASTX with 14-3-3: epsilon isoform 14-3-3 protein (U43430.1)

	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003721
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8045 complex gene
5		appears to encode 3 things : Transcript: CT24102 unknown Transcript CT24072: transcription factor RNA polymerase II transcription factor ,
10		Transcript: CT24092: diacylglycerol- activated/phospholipid dependent protein kinase C inhibitor /14-3-3 protein epsilon (suppressor of ras)
15		
	<b>Human homologue of Complete gene candidate</b>	CT24092: e-119 NP_006752.1  tyrosine 3- monooxygenase/tryptophan 5- monooxygenase activation protein, epsilon polypeptide; 14-3-3 epsilon [Homo sapiens
20		
25	<b>Putative function</b>	transcription factor, or 14-3-3 proteins which associate with cdc25 phosphatases
	<b>Confirmation by RNAi</b>	CT24102: wild type profile only, CT24072: Loss of G1 peak CT24092: Increase of G1 peak



**Example 53 (Category 4)**

5	<b>Line ID</b> <b>Category</b>	951/8 Mitotic defects in brain: (some overcondensation, anaphase bridge, metaphase with swollen chromosome and bipolar spindle)
	<b>Reversion</b> <b>Map Position</b>	NR 73D
10	<b>Rescue ID</b>	2E8S
15	<b>Rescue Sequence</b>	GTATAACAAGATCCCGAGACACCGGTCAGTTGGTGCTACACGCTCTTGGAGA GCGCTGTGTTTGTTCGGTTCAGCGATTAGCGATAGTTTGTTCGAGCCGGTTGT GTTAACTTGGCTAGCTTCGGGTTTATTGTGACACTTTCCCCAAATCGATCGTTT GCGAAGCGTGCATAGCGGAACATACATACATAGATAACCAGCGTGTCTGGGT GTTCATGAAAAAGAGTGCGTGATATGGGATTTCGATATGGCAACACGCTTTATG GATATACTAAAGCTGACCTTTAAGTGAGTTTTCCCAAGTCAGTGTCCGCTTCTTG CTCTTGCGGAGCGTTAAACGGTTTTCTGTGTTTTGAGGTCTCGCGTCTTGGTTT TGCAACAGCTTCTGCCCAGCATGCACACATACGTGTGCACTGGGAAAATAGTG 20 TTGCAGAAAGTGCTTGATTTATAAATATTACAAAAAATGTGATGAAACACTTTT TATTTTCTTCAAAAAATCAAGAATAAATTAACACTATCCTGCTCTTAAACAT GGAGATTAATTCAATTTTAATTAATAAATAATTTTTTTTACAATTTATGATTTA TGAATTTATGCACTCCTTGAAACTATTAAAGACTCAACAGTGA
25	<b>Genomic hit, Accession No.</b>	CSC:AC015272
30	<b>Associated ORF</b>	<b>Genscan ORF1 predicted sequences</b> >23:03:05 GENSCAN_predicted_peptide_1 602_aaMGFDMATRFMDILKLTfKPFKTN YTEEKYFNDKLRSSKNIERRYILDVGRGPTAVTYNPIWVISFKYEQRKLSTAIYSV IKTKSGPVRGVKRNTIWGGSYFSFEKIPFAKPPVGDRLRKAPEAVEPWDQELDCTS PADKPLQTHMFFRKYAGSEDCLYLN VYVKDLQPDKLRPVMVWIYGGGYQVGEA SRGLDVVIVTVAYRLGALGFLSLDDPQLNVPGNAGLKDQIMALRWVQQNIEAFG GDSNNITLFGESAGGASTHFLALSPQTEGLIHKAIVMMSGSVLCPWTQPPRNNWAY 35 RLAQKLGYTGDNDKKAIFEFLRSMMSGGEIVKATATVLSNDEKHHRLFAFGPVVE PYTTEHTVVAKQPHELMQNSWSHRIPMMFGGTSFEGLLFYPEVSRRPATLDEVGN CKNLLPSDLGLNLDPKLRENYGLQLKKAYFGDEPCNQANMMKFLELCYREFW HPIYRAALNRVRQSSAPTYLYRFDHDSKLCNAIRIVLCGHQMRGVCHGDDL CYIF HSMLSHQSAPDSPEHKVITGMVDVWTSFAAHGDPNCESIKSLKFAPIENVTFNFKC 40 LNIGDQFEVMALPELQKIEPVWNSFYAPNKL
45		>23:03:05 GENSCAN_predicted_CDS_1 1809_bp atgggattc gatatggcaacacgctttatggatatactaaagctgacctttaagccatttaaacgaactacactgaagaaaagtattt caatgacaaactcagatcttcgaaaaatattgaaaggcgttatatcttgatgttgcttcgcggaaccacagcagtcacgtacaat ccaatctgggtaataagctcaagtagcagcagcgaattgtcaacagcaatatatccgtcataaagacgaaatcaggctcctgtg cggggagtgagagaaacacaatctggggaggaagctacttcagtttcgagaagatacccttcgaaagcctcgggtgggagat

165

ctgcgcttcaaggccccggaagcagtgaggccatgggatcaggaattggattgcacttcgccggcagacaagccccttcagaca  
cacatgttttcagaaaatacgcgggctcagaggactgcctctacttaaatgtgtatgtcaaagatctgcagccggataaactgcgtc  
ccgtgatgggttgatctacggaggaggctatcaagttggcgaagcttctcaggagtgatgtggtcatagtcaccgttgcttatcg  
actgggtgccttgggcttctcagcctgatgatcccaactaaacgttccggaaatgcagggtctcaaggatcaaatcatggccc  
5 tgcgatgggtgcaacaaaacatcgaagcattcggcgggtgattccaacaatattacactcttggcgaaagtgcggcgaggcctc  
gaccacttcttgactaagtccccaaactgaaggtcttaccacaaagctatcgttatgtcgggcagtggtttgtgcccctggacg  
caaccaccgagaaataattgggcttataggctggccaaaaatgggatacaccggtgacaataaggacaaggcgatcttgagt  
ttctgcgatcaatgagtgggcggggagattgtcaaggccaccgcaacagttctcagcaacgatgaaaagcatcatcggatcctttc  
gccttcggacctgtcgtagaacctatactaccgagcacactgtggtcgtlaaacaaccgcatgaactgatgcagaatagctgga  
10 gtcacaggatacccatgatgttggaggcacgagcttcgagggattgctattctatccagaggttcaaggcggccagcaaccctc  
gatgaggtgggttaactgcaagaatctgtaccgagcgatctcgggtcttaacctagatcccaactgcgtgagaactacggcttgca  
actgaagaaggcgatattcggcgacgaaccctgtaccaggcaaacatgatgaagtttctcagctatgctcatatcgagagttctg  
gcaccctatatacagggcagcttgaaccgtgtccggcaatccagcgcaccacgtatctgtatcgattcgatcacgattccaaact  
gtgcaacgccattaggattgtactttgcggccatcagatcgaggtgttgcacgtgacgatctgtctatatattccacagcatgtt  
15 gtcgcatcaatccgctccgattctcgggaacacaaggtataaccggaatggcgacgttggacgagtttcgcagcccacgga  
gatcccaactgcgaaagtataaaatcactcaagttgcacccatcgaacacgtaaccaactttaagtgtctcaatattggggatcagt  
ttgaagtcagtgcgctccagaattgcagaaaatcgaacctgtgtggaatagttctacgccccaaacaaactgtag

**Drosophila Gene Hit** TBLASTN with ORF1: alpha esterase (aE10) gene (U51054)  
20 **Human Homologue** TBLASTN with ORF1 and BLASTX with U51054: bile salt-  
dependent lipase (S79774)

**Annotated Drosophila genome genomic segment** AE003671  
**Annotated Drosophila genome Complete gene candidate** CG1131 - alpha esterase 10

25 **Human homologue of Complete gene candidate** 4e-48 4557239  
ref|NP\_000656.1|pACHE|  
acetylcholinesterase (YT  
blood group) precursor  
30 >gi|113037|s

**Putative function** alpha esterase

35 **Confirmation by RNAi** Only wild type profiles observed

**CATEGORY 5: SMALL IMAGINAL DISCS (BLOCK TO PROLIFERATION)****Example 54 (Category 5)**

	<b>Line ID</b>	113/20
5	<b>Category</b>	2nd chromosome, small imaginal discs
	<b>Reversion</b>	R
	<b>Map Position</b>	50D/E
	<b>Rescue ID</b>	EcoR1
10	<b>Rescue Sequence 1</b>	
	CTGAGGCNCTTTGCCAATATGTGTATATTGGGCGGGGNACATGCGTNAATCGG	
	TTAAAGCCGCTACTTACATTCTGTTCTTTGCATCTCCCCATCCACAGCTATAA	
	AGCAAGATGAGCTACGCCGCTGATGTGCTGAACTCGGCCCATTTGGGAGCTCC	
	ATGGTGGTGGCGACGCCGAGTTGCGTCGTCCATTTCGATCCCACGGNCCATGAT	
15	TTGGATGCATCCTTCCGCCTTACACGCTTCGCANATCTAAAGGGGCGCGGCTG	
	CAAAGTGCCCGCAAGGAAGTNGCTCCCCCACCT	
	<b>Rescue ID</b>	BamH1
	<b>Rescue Sequence 2</b>	
20	CCACCTGGTACCACAGCGCTCANACGTGTATGTACACGGATTTTCTGCCGCGT	
	GTGTGTAGCGCGGCCCGTGATTGGCTGCAGTCGCGATGGCGGCTAAAACGGG	
	CGAAGTCAGTATTTCTCCCTGTGCGACGANGCGAGCAACGTGAACAATGCCAC	
	TCATTTCAATTGCAAAATGCCAAAAAGTGCGCGCTTTGAATTGGCCATTTGGT	
	TCGTTGCGTTCGTTTGTCTTTTGGTACTTACGTTTGCTTGTGCGATTGTACAAA	
25	GATAATTGTAGAGTAACGTTAGCAAATTATATTTATTTTGCGCCTGGTTTTTGC	
	TTTTCCAACGANCGAGATGTCACAACAGGGTTGTATTANCGTGTGCGGCTGAT	
	TCGATATTTGGGATGCCGATTGTCTGAAGCGANGGTTCAACGGGGCTGCCAAC	
	TCCCCCGAAAATCTATCNATGGTATTGTGCGCCAAGGGTAAAATAAATAAAAA	
	TATGTTAAAACCGCGGAATAAATGGGGGAACCGAAGTGGAAACTGTGGTTCA	
30	CAGTGCTCTGACTTTCGGGAGCAGTTAATATAGTTGGCATTAATTCAATTAGA	
	GCTCCAAAGTGCTGGTCACAAAGAACGCACAAGAACGGGCCATGAAAAACCT	
	GTTGCGCCAGCAGAACGAAAAGTAAAAATTAGAAGAAACCAT	
	<b>Genomic hit, Accession No.</b>	CSC:AC017131
35	<b>Drosophila Gene Hit</b>	rescue sequence: selenophosphate synthetase (ptuf1) (U91994)
	<b>Human Homologue</b>	BLASTX with U91994: SELENIDE, WATER DIKINASE 1 (SELENOPHOSPHATE SYNTHETASE 1) (SELENIUM DONOR PROTEIN 1) (P49903)
	<b>Drosophila EST</b>	LD46437 (AI514756 similar by BLASTN to U91994
40		selenophosphate synthetase (ptuf1) gene)

	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8553 selD selenophosphate synthetase
	<b>Human homologue of Complete gene candidate</b>	1711372 P49903 SELD_HUMAN SELENIDE, WATER DIKINASE (SELENOPHOSPHATE SYNTHETASE (1e-159))
5		
10	<b>Putative function</b>	selenophosphate synthetase
	<b>Confirmation by RNAi</b>	Only wild type profiles were observed

**Example 55 (Category 5)**

	<b>Line ID</b>	121/1
5	<b>Category</b>	2nd chromosome, small imaginal discs
	<b>Reversion</b>	NR
	<b>Map Position</b>	60B
	<b>Rescue ID</b>	BamH1
10	<b>Rescue Sequence</b>	TCCTGTGCACTCATATTGATTTGCCTTGTC AAGTGGCTAAAGAAATATTTAAATG TTTGTTATTTCTGTTGCTAGCGCTCCGACAGTCTGGCAGCACTGCTCGCTGTCG ATAGTTCAACTGAGTTGCTGTTTCATCGAACAGAGCTGCCAACTCTATTTTGT AGCTGGCCAGCCAGGATTGCCAGAGTAAGGCCCTCAAATCAGCTGTTTTGTGT 15 TTTGATTTTATTTTGAAAGTCCTAGTTTAAATTATGCTTTCTCCGACAGATCA GCACAAATAATACTAATAAAGCTCACAATGCTAAGGTTGTGCCTTCCAACTCG AGCTGGATATGTGCGTAAGTAAGGACTTTACGTCTATAAACTTGTTATGTAA AGTAAATGTTTGCCTATTGCGCAATTTCTCCAACGAAAAACCCAGAAAACCNA AACCCCTTNAAANTTTGGAATATNCCCAATGAATGCAGCACCCGTGAAATCC 20 GTAATGCCTTTGTCCAGCTCTCCAAATTGGTAAGTAACTCCAAGATCCAAAGG AGCCTCCTAAACCCTGCCCTTTCCACAGTACCACCCAGATGTTAAGAGCAATG CTGCGTGTCCGGAGCGCACAGCCGATTTGTTTCAGATCTCCGAGGCGTACAAG AACCTGATAAAGCCGGAACGGAAGGAAAAA
25	<b>Genomic hit, Accession No.</b>	CSC:AC020499
	<b>Drosophila Gene Hit</b>	rescue sequence: DnaJ60 gene for dnaJ-like protein (Y11900)
	<b>Annotated Drosophila genome genomic segment</b>	AE003463
30	<b>Annotated Drosophila genome Complete gene candidate</b>	CG12240 – DnaJ60 CG13570 – spaghetti ser/thr phosphatase
	<b>Human homologue of Complete gene candidate</b>	CG12240- 4827026 ref NP_005138.1 pTID1  tumorous imaginal discs (Drosophila) homolog >gi 3372677 (AF061749) 7e- 08
35		
40		CG1116- 2495728 HYPOTHETICAL PROTEIN KIAA0258(aa)
45	<b>Putative function</b>	CG12240 : Chaperone involved in protein folding CG13570 : serine/threonine phosphatase

**Confirmation by RNAi**

CG12240: Marked reduction in G1 and G2/M peaks  
indicating fewer cycling cells  
CG13570: Marked increase in G1 peak

**Example 56 (Category 5)**

**Line ID** 127/2  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** NR  
**Map Position** 57F

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 GCCGGTGGGCCCACACTTGTNCGCCCGCGCATCGGCTGTCTGTGGGAGTGCGA  
NCGAGTCAGATAGTAGATCCGATGCGCTCTCCAGATACTTTTTGAACACTGAA  
GAAAACGCGCAGTTGTGGGTGAATTCAGCATCATCAGATTGAATCACACACA  
ATCCTAGTCGCCTCACGCGAAGAGAACTATGTCATGATCAGATATCGGTGTAT  
GCATTCTATATTATGTACTTCGAAATATGTAATTTATTAAGTTTTCGCTATACT  
15 TTTCAATCAAATTGGCAAAAACCAATTCAAAGGTTTTCAATATTTTCGAAAAG  
CATTTTAGGCTTTCTATGTAACGTATGTTTTCAAACAAAATATTAGTTTTTGA  
AACTTTATTATCGGATAAAACAAATGTAAGCCAAATNACAACGTTNTATGATAC  
TCCCAAAGATCCGCNCTNTTAAAGTGGCCTAAAAATAGCTGACGCATTAANCC  
ATAGGCGCTTCGCTTCTCAAGATAAAACCTGGCGTGCTCAACTCAAGAAACAA  
20 ATATGTGGTTATATACATATATACATATATGGGGCATATAACCGATGTGTGAC  
GTGACATTGGCTCGTTCTATTACATACTTAAACACTAAATGCAAACCTATCA  
AAAACCNACTACACTAAGCGAAAAACGGCAGANATAGTTAAGGAAAGTGGTC  
CA

25 **Rescue ID** BamH1

**Rescue Sequence 2**

CTTCTTTTCTCAAAAAACGTCGCTCGNGTCCCNCAATCGTTTTACAAACTTCGC  
TCGGAACGGACGTGTGCGCGCTCTGAAAGGAAAAAGTGAAAAAGTGTGTGAC  
AAAGTGCAAATAAGCCACAACGCGCATGTGAGAAATCAAATTTAATTGAGAA  
30 GCATCAAAAATTGTATACATATCGAGCGTATCCACATCGCTGTATGTGTGAGT  
GTGCCAGTGCTAGTGTGGTTTTCCCTTTTCGCCGTGGAAAATATGAAAACCTGA  
ATGAAAAACTGAATCGCAGTCAGCCAGAGCCGAATTGGAAAAGAGTAACTCG  
CATTGGGGACACGAAGAGGTGTCTCGAAAAAGGTAAAATCTTTTACACAGAA  
ACGACGCCAGAAAGCGATTAGCGATTINTGACTATGTGTGAGTGTGTAATTC  
35 GGTCTACGGCTGTGTGTCTGCATTTTATTTAACNTTTTGTTCCTCCNGTTNGNTC  
CACNGTAAAAATAGCTAAAAAAAAGGGCAAGTACTCTTGGCGCGCTCTCCC  
TCTCTCTTTGTTGGTCGTGACTGCGACGTCACCGTTCACGTAGAATCGTTTTCA  
AGTGGCGTTTCTTTCTTTCTTTTAAATGTGCTGCTTCTTGCTTCTGCCTCTTCTTC  
TTGCCTTTGGCTATCTGCTTTGTTTTGAAATACGTCCATGTTATTCCAGTGTCTG  
40 TGCCAAATGTGTGCGANATGATCTCTACTT

**Genomic hit, Accession No.** AC009732

**Associated ORF**

45 Genscan ORF1 predicted sequence  
>/tmp/aaaaafra|GENSCAN\_predicted\_peptide\_2|456\_aa

171

- MQTKGPITDADCIRGMACRALAGLARS DRVVRQIVSKLPLFASGQLQTLMRDPILQ  
 EKRAEHVIFQKYALELLERVSGTKPLNNPLDPSLSNMHKANVIAQTRIQYNKQQ  
 LYQLIFEHLESNGLSQTAQMLQREVGLPLQTPTRSFHQSPFDYKSLPSGSSSLSRN  
 RLRSRMQDVNAAIMGNGLNRSFGEDSSPAGAGGSNAGDGVSPNPFSSSLNTTQTP  
 5 IKIRRTDRSSVSRSIQKQAMEPGGMSVGLAEDGQLHPKRITLNTIVTEYLTNQHSL  
 CNNPVTTCPQFDLYEPHKCPDPKPSRLLSSNYNLTSRHARTQAGFNTSRFDRRYV  
 HTHFSPWRSIRSADYEDLEFTCCDLAGKYIIVGTQQGDGRVFNMNDGVEQFFSNC  
 HNFSVDAIKANRAGDLVITSSFWRTPTSILWSIADDEFKLKLRLPDVITYCEFSQTV  
 QDRLLGTQNEVY  
 10 >/tmp/aaaaafrla|GENSCAN\_predicted\_CDS\_2|1371\_bp  
 atgcagaccaaaggaccattacggatgcggactgtatagtggaatggcctgtagggccttggcgggacttgctcgtccgatc  
 gggtcaggcagatcgtcagcaagcttccactcttgcagcggacaactccagacgctgatgcgggatcccatactccaggaga  
 agcgcgcggaacatgtaatctccaaaagtacgcattggagttgctagaacgagtgctcgggtaagacgaaaccgctaaataatcc  
 15 ttggtatccatcgtgtccaacatgcacaaggccaatgtaatgccagacacgcacatccagtataacaagcagcagctgtatcagc  
 ttatcttcgagcaccttgaaagcaacggctctctccagacagcccaatgctgcaacgggaggtgggtcttccgctacagactcc  
 cactacgcgcagtttcatcaatcaccttccgactacaaaagcttccagtggtagtagctcgtgtctagaatcgtctcgaagc  
 cgcatgcaagatgtgaacgcagcagataatgggcaatggagacttaaacagaagtttggtaggactcctcgcggcagagacc  
 ggtgtagcaatgcgggagatggagtcagcataccaaatttagctcccttaacacaacgcagacgcccataaaaaataaggagg  
 20 acggatagaagttcagttagccgctctatccagaagcaggcaatggagcctggtggcatgtcagttggtcttgcgaagatgtca  
 actgcatcccaagaggatcaccciaataaccatcgtaacggaatacctcaccaaccagcactcgtgtgcaataatccggtgaca  
 acctgcccgcagtttgattgtacgagccgcacaagtgtccagatccgaagcccagccgattgctaagctcgaactacaacctga  
 ctatcgcatcgtcgaacccaagccggatttaataaccagtcgtttgaccgtcgtatgtgcacacgcactttaccatggcgta  
 gcattcgtatcgccgactacgaggacataggttcacctgttgcgatttggcgggtaatacatcattgtgggcacgcagcaggg  
 25 cgacggacgagtggtcaacatgaacgatggcgtggagcagttcttccaactgtcacaactttagcgttgatgtatgaaggcta  
 agagccggagacttggtcatcacatctagcttctgcgccacacccaccagcattctatggtctattgcggacgatgagttcaagcta  
 aagttgcgacttccgatgtcacgtactgtgagttcagtcacaacggtgcaggatcgttggggcaccagaatgaggtatactaa  
 corresponds to CG10082  
 30 *Drosophila* EST      several including SD04293 (AI532704)  
 Annotated *Drosophila* genome genomic segment      AE003454  
 Annotated *Drosophila* genome Complete gene candidate CG10082 – novel protein with  
 35 homology to enhancer Pi uptake  
 Human homologue of Complete gene candidate      1665793 dbj|BAA13393|  
 (D87452) Similar to  
 40 *S.cerevisiae* YD9335.03c  
 protein (S54640) [Homo  
 sapiens] (2e-43)  
 45 **Putative function**      Putative phosphatase or enhancer of Pi uptake protein  
**Confirmation by RNAi**      Reduced G1 and G2/M peaks indicating fewer cycling cells



**Example 57 (Category 5)**

**Line ID** 131/8  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** R  
**Map Position** 60A

**Rescue ID** BamH1

**Rescue Sequence 1**

10 CACGATTGCNNGGCCCATCGAAGTGTGGGTCTATCGATACTCGTGGGTAAATAA  
ACAAGTTCTGAACTGCGATTTTCGGGGGTTTGAGGGGTCAATTGTCCCCTGTGT  
TGGAATGTGTTCTAAATCTACACAAACACTCCCTAAGCTTATCCTAAACTTAT  
AAATATTGGTTGCTATTTAAACCCCATTTACGGTTATCCAGCACGCCCCCTGA  
ACTGTGACCCACATCCCCGATTTTAGTGACTAGTTTATACTTATCGTGGTTGG  
15 CATTTGGTACACTACACTTTCTTATTCACCTAGATCGCCGACTCCGCGCACGGT  
CGCGCTCCCGTTCCCGCTCCCGATCTCGGCTGCGACTGCGGTGCGGATCCCGTT  
CCCGGTGCGGGCGACCGGCGCCTCCANATCCGGATCCCTAANCGGCANCNCT  
CNTGGTGGCAATCNNGGAATGTTCCGGGGNCCNCTACCNCAGTGNAATCAC  
TGGTACGTCCCACCGCNAAACTCCGCCANTGCGGTTGCCGGAACGGGTGGC  
20 ANTGCCAATGGGTGCTGCAGAAGGTACCATCACAGCAATCGCTCACGGANC  
CCGAAGACTGCCTCTGCCGCCCGGTGGGCCACTCATACACGCTACACGGTCG  
GAAATACTACATTGATCACAATGCGCATACCACGCACTGGAATCATCCGTTGG  
GAACGC

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

AATTGATTTCCGGACATATAAACAGAATCCAGAACTCATCCGGCAGCAGGCTC  
AGTCAGGCCAGTAAATCCGAAAAGAGAGTAACCAGCAGGAAAAGAGAATCC  
ACGTAAATACAGAGAAAATGGCTCTACGCGTCCAATTCGAGAACAACGACGA  
30 CATCGGCGTATTCACTAAACTAACCAACACATACTGCCTGGTGGCCATCGGTG  
GATCCGAGACCTTCTACAGCGCCTTCGAGGCGGAGCTGGGCGACACCATCCCG  
GTGGTGCATGCGAATGTGGGCGGCTGCCGGATCATCGGCCGCCTCACCGTGGG  
CAACCGCAACGGCCTGCTGGTGGCCAACTCCACCACCGACGAAGAGCTGCAA  
CACCTGCGTTACANCCTGCCANAACCCCGGAAANATTTATCGTGTGGAAGAAC  
35 GCCTGTCCGCGCTGGGCAACGTTATCGCCTGCAATGATTATGTGGCCCTGGTG  
CACCCGGATCTGGACAAGGAGACCGAGGAGATCATCGCGGACGTGCTCAAAG  
TANANGTCTTCCGCCAGACCATTGCCGACAACTCACTGGTGGGCTCTTACGCC  
GTGCTGAGCAACCAGGGGGGCATGGTGCATCCCAAGACNAGCATTACAGGAAC  
AGGACAACCTGTCGTCCCTGCTGCAGGTTCC

40

**Genomic hit, Accession No.** CSC:AC020517

**Associated ORF**

Genscan ORF1 predicted sequences >22:13:05|GENSCAN\_predicted\_peptide\_4|357\_aa  
45 MALRVQFENDDIGVFTKLNTYCLVAIGGSETFYSAFEAELGDTIPVVHANVGG  
CRIIGRLTVGNRNGLLVPNSTTDEELQHLRNSLPDAVKIYRVEERLSALGNVIACN

173

DYVALVHPDLDKETEEIADVLKVEVFRQTIADNSLVGSYAVLSNQGGMVHPKTS  
IQDQDELSSLLQVPLVAGTVNRGSEVLAAGMVVNDWLSFVGMNTTATEISVIESV  
FKLNQAQPATVTTKLRAALIEDISRSRVAGGGGGGGGGSSSGNSSSGPSTSRRTT  
5 RNNAAATAADRPKINEADLEGKSPEEVEMLKTMGFCTFDTTKNRKVEGNDVGEV  
HVILKRKYRQYMNRRKGGFNRPLDFVA

>22:13:05|GENSCAN\_predicted\_CDS\_4|1074\_bp

atggctctacggtccaattcgagaacaacgacgacatcggtcttactaaactaaccaacacatactgctggtggccatcgg  
tggatccgagaccttctacagcgcttcgaggcggagctggcgacacatcccgggtgcatgcgaatgtggcggtgccc  
10 ggatcatcgccgctcaccgtgggcaaccgcaacggcctgctggtgcccaactccaccaccgacgaggagctgcaacacct  
gcgtaacagcctgccagacgcgtgaagattatcgtgtggaggagcgctgtccgcgctgggcaacgttatcgctgcaatgat  
tatgtggccctggtgcacccggatctggacaaggagaccgaggagatcatcgcgacgtgctcaagtagaggttccgccag  
accattgccgacaactcactggtgggtcttacgccgtgctgagcaaccaggcgccatggtgcatcccaagacgagcattcag  
gaccaggacgaactgtcgtccctgctgcaggttccctcgtggcggaacagtgaaccggggcagcgaagtactcggcccg  
15 gcatggtgctcaacgactggctctcctcgtggcgatgaacaccacggccacagagatcctcgtgatcgagagcgtcttcaagctt  
aaccaggcacagcccggccacagtgcgacgaagctgctgctggccctcatcgaggacatatcgcggtcgagggtcgccgga  
ggaggaggaggaggagcgccggcggaagcagcgccggcaacagcagctccggaccatcgacgtcggaaggacgacg  
aggaacaatcgccggccacagctgcccggcccaagatcaacgaggcgacgtgagggttaaatcgccgggaagaggt  
cgagatgctgaagacaatgggattctgcacgttcgacaccaccaagaacagggaaggtcgaggggcaacgatgctggagaagtg  
20 atgtaatcctcaagcgaagtaccgccagtacatgaatcgcaagggtggcttcaaccggccgctcgatttcgtggcatag

**Drosophila Gene Hit** rescue sequence and TBLASTN with ORF1: b(2)gcn  
(EUKARYOTIC TRANSLATION INITIATION FACTOR 6  
)((X97641)

25 **Human Homologue** BLASTX with X97641: integrin beta 4 binding protein (HUMAN  
EUKARYOTIC TRANSLATION INITIATION FACTOR 6)  
(NP\_002203.1)

**Drosophila EST** GH08760 (AI109537 similar by BLASTN to X97641  
"D.melanogaster b(2)gcn gene." )

30

**Annotated Drosophila genome genomic segment** AE003462

**Annotated Drosophila genome Complete gene candidate** CG17611 – bcgn benign  
gonadal neoplasia homology  
to Eif6 translation factor

35

**Human homologue of Complete gene candidate** 6016331 EUKARYOTIC  
TRANSLATION  
INITIATION FACTOR 6

40

(EIF-6)(aa) and 4504771  
|ref|NP\_002203.1|pITGB4BP|  
integrin beta 4 binding  
protein(aa)

45

**Putative function** eukaryotic translation initiation factor 6 (eif-6)(aa)

**Confirmation by RNAi** Slightly reduced G1 and increased G2/M indicating block in  
G2/M

**Example 58 (Category 5)**

	<b>Line ID</b>	135/25
	<b>Category</b>	2nd chromosome, small imaginal discs
5	<b>Reversion</b>	NR
	<b>Map Position</b>	24A
	<b>Rescue ID</b>	EcoR1
	<b>Rescue Sequence</b>	
10	ATAACATGGGCNCTGGTTTTTAAGTNAAGCTCTANTNATTGGCCCCCATTCTTA NNCTCTCTCGCTCTCTTCTCGCTCTTTCGCCTGCTCTCTCGCCTGATTATTCTGC TTGGTCGGCTGATGGTTTTTNGTTTINATCTGGTGTATTTCTGCGTAGTTTATG ACAAACCGGCTGGTTCTTGTGTTATTGCCGTATTCTAATATATTTCCCCTATTG TTCTTATTTTTGTTGCAGCCTGCACACCTCGGAGGTTCTAGATGATAAGGGGTG 15 TAGCGATGGTGGGGGGCTGTCTTGANGGGCTTCTCGCCTGAGCTCTTGTTTAT CTTTGGTCATTTGTTATTGTTTAATGCACGGCAATATTATTGGTAAACAAGTTA GCCAACAGCACTAAACGCCAATCGCATTCTTTCTAAAAACCAAGTCTATTGT CGATCTTGCTAGGGAATGATGATGACTCAGGTGCAATTGGGATCTTATCTAT GGCTGTCTGGGAATCAAGAAGTGTTCCCGCAGAATTCGTGAANTACTGCCGCT 20 CTCTCCATGGGGCCATTATTTGCACTCGTTTTNCGCGAAATACCATNAATTAGC ATAAAGACACGTCGCCGGCAATCGTGACGTAGGCTATNAATGCCTTCTATGCA TGTGCNAACTCGCGGAAGCATAGCAATTTGAAGGAACAATTTTCANTGCAG GTTTTAATGGGCTAAAAAA	
25	<b>Genomic hit, Accession No.</b> CSC:AC014199	
	<b>Associated ORF</b>	
	Genscan ORF1 predicted sequences >20:54:54 GENSCAN_predicted_peptide_3 117_aa MSASPTARQAITQVMPMITRKVVISDPIQMPEVYSSTPGGTLYSTTPGGTKLIYER 30 AFMKNLRGSPLSQTPPSNVPSCLLRGTPRTPFRKCVVPTELIKQTKSLKIEDQEQQF QLDL	
	>20:54:54 GENSCAN_predicted_CDS_3 354_bp atgtccgcttcacccaccgcccgtcaagccatcaccagggttatgccatgatcaccaggaaggtgtcatctcggatccgatcca 35 gatccccgaggtgtactcctcgacgcccggcgaacccttactccaccactcctggaggcaccaaaactatctacgagcgggc tttcatgaagaatctcgtggctccccattgagccaaactccgctccaacgtgccagttgctgctgaggggaactccgcgta ctcccttcgcaagtgcgtgcccgtcccacggaactgatcaagcagaccaagtcgctgaagattgaggaccaggaacagttcc aactggatctgtag	
40	<b>Drosophila Gene Hit</b>	TBLASTN with ORF1: BcDNA.HL08053 mRNA (AF132557 )
	<b>Human Homologue</b>	TBLASTN with ORF1 and BLASTX with AF132557: eukaryotic translation initiation factor 4E binding protein 2 (EIF4EBP2) (L36056)
45	<b>Annotated Drosophila genome genomic segment</b>	
		AE003579

	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG8846 - phas1 translation initiation factor 4E binding protein 2
5	<b>Human homologue of Complete gene candidate</b>	CG8846 - 4758260 ref NP_004087.1 pEIF4EBP2  eukaryotic translation initiation factor 4E binding protein 2 (4e-16)
10	<b>Putative function</b>	EIF4E translation factor binding protein
15	<b>Confirmation by RNAi</b>	Slight reduction in G1 and G2/M indicating fewer cycling cells

**Example 59 (Category 5)**

**Line ID** 141/12  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 21A/B

**Rescue ID** BamH1

**Rescue Sequence**

10 GGCTCTTTTCCAAANAGGCAGTTTCTTGNCCCATTCTTGGATTGCTTTGTAGT  
 GAACTNAATCGTTTTGTTGGTTCCTCTGTCGTCCAGTCTTGTGAAAATTCGTG  
 ATAATAATGCCTGGATAAATANTTAAGCATTGGAACCGGGGAAAAAGGG  
 CTAAGTTGTGTGAAGGAAACAATTGAAGTGACCCTTTGTNTATAAACATTCCA  
 CGACGTGTTTCGAAAAACAAACAAAGATATGCGGAAACAAAGTGTTAATAAAA  
 15 GAGCNAAAAATAGAGAGAGAGTGTGCGGATAAGCGGTTGAGCGAGATAGAG  
 AAAATTGTTGATTAAAAATGTGTGTCNAAATAAAACATCAAGCCGCTTGAACGA  
 ACAGTCAGTTAGTTGCTTCTGATAATAACCATGGGAAGCGGCNCGTGTGCTTC  
 GCTCCTCGTTACTTATAAAATATTTAAACGTTTGCAATTCTTCNTATTTCCGAAT  
 TTTTGCNCCCCTGAANCAACTTNGTTAAACTGCAAATAGCAATGCAAACAAAC  
 20 GAATAGAAACTGAAATCGACAACNACATGTGAAATTCACAAATCAAATCGCA  
 ATTGTCATCCCAAAGATATAGAACAAGCTATAGGGAAGATANAGAATGTAAG  
 TGCCAAACTAAAAATAACAAACAAGAATAACATTTCCACAGGTGTTTTGCATT  
 TCAAATGCATATTTCCGTGGCGGNTACAAATCTTTTCAAAACCG

25 **Genomic hit, Accession No.** CSC:AC017815

**Associated ORF**

Genscan ORF1 Predicted sequences >17:48:30|GENSCAN\_predicted\_peptide\_2|554\_aa  
 MSNKKMFNRRTTSVSPGQLHYHYHTDFYYSMPDLHKTRKMHGVKRVLVFCLMIVIL  
 30 PAILIIMPLHLRKTVFADVYPMAESDIEIRAGISSIFCSKHTLRMNSNFNAFQLRNL  
 PEIATNRKHRLKKSMTLPDDTLEYWGFFLLKGAKVRVKFCSRYDGSRLIIHGHR  
 ELNLCLGLTDHNKNKLGANYAKGHEQVQVFFEDNVEITEEKGNDQVLMENHNHG  
 GEDLTEDIPQPQVNIPVKQNNSIQPKLIRKKLKGTHHGEHDMHAITDLQGSHTT  
 EHILNHHDHSSNSPAHHHNSTAHHREHSSNITNEETSRNHIRNEDEDPDQNSSKTH  
 35 YSAESPPIRERLKRHNRAHRNQKRQDLYDTLYKRSKRENVYDRKTIHGGNAIN  
 FTETDESNSVSSFETGLFQCFNGMILLQEFFRPKNECSNPHIMDTSPNKSSMVVHN  
 VIEDGYYYYIFYSDNDHVQNEIHAFDIYKPTYQYSNMSESQSCLNTTNCTFNISFL  
 SDEIVVVEVPTRDIEHEEDDITNLISTCHPRSEIYAIFPITVLVLILCCSFL

40 >17:48:30|GENSCAN\_predicted\_CDS\_2|1665\_bp

atgtccaacaaaaagatgtcaacaggactacgtcagtaagtcctggacagttgcattattatcacaggatttctattactcaatgcc  
 ggatttgcataaaacccgcaaaatgcacggcgtgaaaagggtgctggtttctgctgatgattgtgatactgccggccattctatc  
 attatgccgctgcatttgcgaaagacggtgttgcgacgcatcatccatggcggagtcgatacattgagattcgggcagga  
 atctcgtcgatcttttctcgaacacacacatgcgtatgaactcaattcaacgcttttcaactacgtaataagccggaattgcgac  
 45 gaatcgcaagcaccattaggctgaagaagtcgatgacattgccgatgatacgttgaatactggggcttctcttctgctgaaagggtgc  
 caagggtgcgagtgaattctgctccgctacgatggatcccgatcctgatcatccatggtcacagggagcttaattcttgcggtct

177

gaccgatcacaataagaataagtggcgccaattatgccaaagggtcacgaacaggtgcaggtgttcttcgaagacaatgtggag  
 atcacggaagagaagggaaccaggatgtgctaattggagcacgagaaccacggcggagaggatttgactgaggatattccaca  
 gccgcaggtgaacatacctgtcaagcaaaacaattctatacagcctaagtaattaggaaaaaactgaaaaagggcacaattcatc  
 atggcgaacatgatatgcatgctataacagattgcaaggatcacaccatacggacacatatattgaatcacatgatcacagctcta  
 5 attctccagcacatcatcacaatagtagtacctatcgggagcacagttcgaatatcacaacgaagaaactagtctaatcaca  
 tacgaaatgaagatgaagatccagatcagaattcaagtaagaccattatagtgcggaaagtccgcctcaccgggaacgtctcaa  
 aagacacaatagggtagcccataggaatcagaagagacaggatctttacgatacgtttataaaagatcaaaggaggagaatgtc  
 tacgatagaaagacgatccatggaggaaatgctataaattttacggaaacggacgagtcgaattcgggtgtccagctttgagacagg  
 actatttcagtgtttcaatggaatgatcctgctgcaggaggttcttcaggccaaaaaatgaatgctcaaatccgcacataatggacactt  
 10 cgcccaacaagagttccatgggtgtgcacaacgtcatcgaggatgggtactactattatattctacagcgacaatgatcacgttc  
 aaaacgagatccacgccataitcgatatttacaagccgacgtatcagtactcaaacatgagcgagtcacaaagctgtctgaatacc  
 acaaattgcacattcaacatcagtttccttcggatgagattgtgtgtggaggtccaacacgggatggatcgcagcacgagga  
 ggacgatataaccaatctgatctccacctgtcatccgcgcagcgagatatagccatctttccattacgggtgctggtgctgatcctt  
 gctgctccttctgtag  
 15

corresponds to CG9524

20	<b>Annotated <i>Drosophila</i> genome genomic segment</b> <b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	AE003623 CG9524 - novel His-rich protein
	<b>Human homologue of Complete gene candidate</b>	none
25	<b>Putative function</b>	No homologies which indicate function
	<b>Confirmation by RNAi</b>	Reduced G1 and G2/M peaks indicating fewer cycling cells

**Example 60 (Category 5)**

	<b>Line ID</b>	146/2
	<b>Category</b>	2nd chromosome, small imaginal discs
5	<b>Reversion</b>	NR
	<b>Map Position</b>	26B
	<b>Rescue ID</b>	EcoRI
	<b>Rescue Sequence</b>	
10	TTTNATCCAAACTGAGANACTNTTGGCCCCAAAACTGAAAACTCGGACTCGGG	
	CGCGTAAGGGAGTCGGTCNTCGGGAGTCGGTCGTCTTTTGTGATCTTGAGAC	
	TGAAATTCCAATTGTTGATTTATCTCTCGGCTGCTGCGCCGCGGCTGCGCTGCT	
	GCAGCGCAGTCCCACTCCGATTTGACCAGCGACCAAGTTTATAAACTTTGAG	
	CCAAAATGCAGCGGCGCACAGTTGTTACCAAAACGTTGCACGCGTCGTGGCCC	
15	TCATCAAAACAAAAAAAAAAAAATATAAGCGAAAATGAAAACGAAATTCGGTTA	
	ACGTCAACAGAAGCTGACAAAAGGCAGAAAAGACCGAAACAAGTTGCAGGG	
	CCAGAGTAAGCCAAGTTAAATGCGAAAGAGAAGCAAGAGNCAAGAAGAAAN	
	AATGGGCACTACATACATATATTATAGCCAGCTAATCTGTTGTGCAGTGCATT	
	TTATCAGCCNCGAAAAGAAAACGAAAACGAAAAGTCGGTCCAAGTTTCGGAC	
20	TCAAAATCCAAACAGAAGAGACTCCATNCCATCAGAGACACGCGGATCTCAT	
	CTCGGTAATGTCTCAATAAAAAGTAATCTTAACTGCCGCCGGAATGTTGAAA	
	AAGTGAAAATTGAAGCGCTTAACGTGTTTCGAAATACGATACATGAGAAGTCC	
	CAAAAAAAAAA	
25	<b>Genomic hit, Accession No.</b> CSC:AC019865	
	<b>Drosophila EST</b>	GH19286 (AI388389)
	<b>Annotated Drosophila genome genomic segment</b>	AE003481
30	<b>Annotated Drosophila genome Complete gene candidate</b>	CG11353 - novel with weak homology to sugar acetylase? CG7525 - tie receptor protein tyrosine kinase.
35	<b>Human homologue of Complete gene candidate</b>	CG7525- 4e-23 4557869 ref NP_000450.1 pTEK  TEK tyrosine kinase, endothelial >gi 464868 sp Q02763 TIE2_
40	<b>Putative function</b>	Sugar acetylase and receptor tyrosine kinase
	<b>Confirmation by RNAi</b>	Both gave a reduction in G1 and increase in G2/M peaks indicating arrest in G2/M

**Example 61 (Category 5)**

**Line ID** 155/13  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 21B

**Rescue ID** BamH1

**Rescue Sequence 1**

10 GNTTTAGTCCNCTTTTGANAGGGNCTTGGNGNCTTAAANAANNAAAAAAGGG  
 GNCCCGGCNCCCAGCAAANAGNNTAAAACTTGAATGGTTTAATTCGAAAATC  
 TTTTAGAAATGTGCGCTAATACCTTATCGGTATAGAGTTCACCTCGTCTCCTAA  
 TCCATATTTTAAGATATCAATATCTATTAACAATTTTATCGTATGATTAGAAA  
 TTCGCATTGTTTTATTATTTTCGACCTTTGGGCTTTACATCGACAGCTACTCTCTA  
 15 TCCAGACAGGAGACTGGGAGAGAGAGCACGATGCTGTCTGAAAGCATGAATG  
 ATGGATGCTGTGCCTATGTGCGATATGCACGTTGCCTGAGCTAAAACGAAACG  
 AGATTATTAATCTATCCGCAAGATTGAGATGCTGATTCCACATGAGTGAGCGA  
 GTCCGTGAGTGGATATTGCTCTCTCCGAAATGCATGCATGAGTGAGCAGGGGG  
 GCTTCAATCGCNCTNTCGATNTGCGACAGNGACATNTTTTATCTTCGACNAT  
 20 GCNCTCNCTCCCTCCCACAGAAATCTTGCGCTNGNTCTCCGANNTNGGGNTNG  
 ANGGCNCTCTTCTCTNTCCTTAAATTGGGANTTNNCTTTTTTCNAANAAGGGN  
 NAGA

**Rescue ID** EcoR1

**Rescue Sequence 2**

25 AATCNTTTTNTCCATTNGGCGNCTTNTCAAAACATATTCACATTTGGNCCCAA  
 CGGCGTANGACTTNATCTCACGATTGTTTGGTTTCCTACTCTCCCGCGCTCCCT  
 CTCTTCTGAGTCTCTTTCTGGCTGATTGCGATTTCGATTTTAGCCGCTGCCATCG  
 CCGTTGTTTGCCTACCTATGTGTGTGTGTGAGGAGTGTGTCTTGATTTTCAGT  
 30 CCGCAATGCGCTCCGCTCATTATTTGTTTGANCGCCGCGGTGTAAAGTTGTAA  
 AAAGTCCAAGTGCTCGTGGAAGCTCGATGCAAGACGGGGAAAACGAAACGCG  
 ATAAATCGTGAGAAAAAGAGAGTGCGCTAAAGGAAGAGGGAGTGATAATCAN  
 ACGAAATGGAATAATGTNTTGCAGAGGCNACAACAACATGCAAATAGTTG  
 TCATTGAGGCGCAATGAATGATAATTAGTGCTTANTTGAAATCATAATCNTGA  
 35 AGAAAGCGTAAAGCTCGATTNTGGCAATNTATTCTTGATTACCANTGAGTCTG  
 TGATATTGCCGTGTGTNCCGAAAATGGANGTTATNAAACCCATGGACTTCAGC  
 ACCTTCTCCGCGTTCTGCGAACATCTTAACAAATCTCCACAAAATTGCAGCAA  
 CAACTGCANCGACGGTACCGCCAATAAANCAATGGAAAANGCATTATTTG  
 GAGGTAANAGCNAAAAATACCAATNTTCCAATGCGAAATTGCNAGCNTGG

40

**Genomic hit, Accession No.** AC004274

**Annotated *Drosophila* genome genomic segment** AE003590

**Annotated *Drosophila* genome Complete gene candidate** CG13693 - novel

45

**Human homologue of Complete gene candidate** 6e-05 4507659 translocated



180

promoter region (to activated  
MET oncogene)  
>gi|1730009|sp|P12270|TPR\_  
HUMAN POOR MATCH

5

**Putative function**      No homologies to indicate function

**Confirmation by RNAi**      Only wild type profiles observed

**Example 62 (Category 5)**

**Line ID** 162/24  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** R  
**Map Position** 55C

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 TTTTNTTTCANGGNTCTTTGCNCATAAAAANACACGNGCCCTCNTGTCCATTTCAC  
ATTTTACTTGGAGTCGGTAACGTTGAGTTCCGCGTCCGTGCGTTCTGCCTTCCA  
ATACAAAGTCTGGTGTGAATCTACCAAGCATTCCAGTGNGAAAATCAACTCAC  
ATTGCTCGGTGATCCNTGCGGCGGTATNATCGCACCCGGAATTGCATAAGTTG  
CGGNGAGCGGAAAGAGAGTGCACGGATTTCNGTTATCNAAGGGCCGGCANC  
15 NGTGGGGCGGCGACGGNAGAGCACGCAGAANAANAATANANTGNNGTGGCG  
AATTNAAAAATANNATNAAAGAAAATTCGGGCGCGCTAATTTTTCTTCAAATTT  
GTGTGCGGTGCGCGA AAAACAACGTGTTTTCNATGGTTGATAATACACACGG  
ACGGNNCACTCGCGCTCACCCACATAGTCACNAAAGTCGGCGACGTCGACGA  
CCNCACNCTCACATANGGACNTTTAATCCCGTNCATNCGTGTAGCGTNCNTA  
20 TTTAACCNTNTCTGTCCATCGGAACGCNCGCNTTCTCGCCTTCNTTCTNCTTTA  
CTTTAATTTCTATTTNNAAGGGGNAGNCCNATCTTTTNCCTNTCNNTGCCNT  
TTAANNTCATCCACANCTCNCTTTNTCNTTCCCTCCNCCTTNTNTCTTTTCNTC  
TTNCTTNTGNCCTTGCCCTCGTCTTTCTCTTCNTCTCCTTNCCCTTCTCCTCCTTT  
TTTCTCCTTCCCCC

25

**Rescue ID** BamH1

**Rescue Sequence 2**

AAGNCNCCTTGGCCGNNTTNAACGGNAANTAANCCGGGNCNCNCGGNCNCGA  
TAATCAGGTCNANCCTTGTGCCTACCACCACCAAATTGAAAAAGAGCNAAGA  
30 TTCTCTAAGGCAAAAACTCCCCAATCTGTGGAATTTCCGGAAGCGAGAGCAC  
ATTCAAAGCTACCAGTTATCAGCGAGCAGCATGTCTAAGCTCAGGAACCTGTT  
GCCCACAATCTTTGGCGGGAAGGAGGCACAGAATCCGACACCCGTCGAGGGA  
CGCCTGGAATAGGACGCAGCTCCCGTGGACGACAACGAACCNGATTACTACT  
ACTGCGGAGCCATGGCGCTGCCCTCCACCGCTGGCACGCCCACAGCCTCCTCG  
35 GATCTGACCGAATCCGTGCTGCGCGAGCTCAGCGACCCAAACTACAATTCAAT  
GGATGTGGTGCTTTTCNNCCTNTTTTCCGGGCACTCTCAGTAACGTCCAGACAA  
ACAACACCATGAACGTTACNCGCGCCAGCAACAGGTGGTCATGAACCTTCTCG  
AATGCCAATAATCTGCACTTCGGCTCCGTCTTCAACTTCAACCAAACTTGAG  
CGCCTGCNGCTCNCGAANGGGTTTACCNGTTCGCANAAGAATCGGTGCGCTC  
40 TCCANACNGT

**Genomic hit, Accession No.** CSC:AC012981

**Associated ORF**

45 Genscan ORFs: ORF2 predicted sequences  
>18:26:17|GENSCAN\_predicted\_peptide\_7|1320\_aa

MEETNNATTIEQQPIALINGQEQVANEQQPSSPTSVATPTSTTSGGTGNATPAFSY  
 DDLFPALPANTS AQSGASGSLARVTSSQKTHIVHVPCKERKSTESEKFGESES  
 KRICQKITKETGAQIEIASRQVTVPREHFRVILGKGQRLREIERVTATRINIPSQSD  
 ESEFITIAGTKEGIAQAEQEIRQLSAEQYKKSSDRITVPKVYHPFIVGYPYSENLNKLQ  
 5 EETGARINVPQQVQKDEIVISGEKDAVAAAKAKVEAIYKDMKKCSTVSVEVAK  
 PKHRYVIGPKGSTIAEILQLTGVS VEMPPNDSPSETITLRGPQVALGNALT VVYQK  
 SNSVKSVEINAAHWHKYVFGRKGANMKQLEEDCPNVNVCLEDKIKLEGDPEN  
 VDRAVAYLSEIKNYEENFTFEVMTVNPSSYKHIIGKAGANVNRLKDELKVNINIE  
 EREGQNNRIEGPKEGVRQAQLELQEKIDKLENEKSKDVIIDRRLHRSIIGAKGEKI  
 10 REVKDRYRQVTTITPTQENTDIVKLRGPKEDVDKCHKDLLKL VKEIQESSHIEVPI  
 FKQFHKFVIGKGGANIKKIRDETQTKIDLPAEGDTNEVIVITGKKENVLEAKERIQK  
 IQNELSDIVTEEVQIPKYYNSIIGTGKLISSIMEECGGVSIKFPNSDSKSDKVTIRG  
 PKDDVEKAKVQLLELANERQLASFTA EVRAKQQHHKFLIGKNGASIRKIRDATGA  
 RIIFPSNEDTDKEVITIIGKEESVKKAREQLEAIKECDEVTEGEVSVDPKHHKH FVA  
 15 KRGFILHRISEECGGVMISFPRVGINSDKVTIKGAKDCIEAARQRIEEIVADLEAQT  
 IEVVIPQRHHRITIMGARGFKVQQVTFEFDVQIKFPDRDATEPVEGLTNGGSGENG  
 GENEGQGEQEVEKEAEQEPVRQCDVIRITGRIEKCEAAKQALLDLPIEEELSVPF  
 DLHRTIIGPRGANVRQFMSKHDVHVELPPSELKSDVIKVCCTPARVAEAREALVK  
 MIEDYEADRADRELRSFVLQVDVDTFHSKLIHRHGA VINKLRADHDVVISLPKRD  
 20 EPNDRIISITGYQANAEAAARDAILEIVGDPETLHREVIEIDKRIHPLIGQRRRTIRKII  
 EDNKVNIKFSADDDNPNISIFISGKIEDVENVKELLFGMAEDYERDYL DNVAIAPPTI  
 GAFLTGFWIRCRRCQRRERIRHQRRTVGEAKAGQKPDCAQHSVAGGLPALRCWRG  
 SGGHLA YHLRVGPQKLSASGRVSRSPA VAAILQVGVRRGSELEMDQELEQKLELE  
 LEDYRAMSGRAAAVVRTSL

25

>18:26:17|GENSCAN\_predicted\_CDS\_7|3963\_bp

atggaggaaactaacaacgcactaccatcgcagcagccatcgctctcattaatggccaagagcaggtggccaacgagca  
 gaaccatcctcgccaactcagtgccacgcccactagtagcggcggaactggcaatgccacaccgccttagctac  
 gacgacctgttccggccctgcccggccaacacttcggctcaatcgcaatcggagcttccggttcgactctagctcgtgtgacgag  
 30 ttcccaaaaaactcatattgtgcatgttccctgcaaggagcgcaagtcacggagtcggagaagtgtggcgaaggcgagtcgaag  
 cgtatttgcagcagatcaccaaggagaccggagccagatcgagattgccagtcggcaggtgaccgttctcgggagcacttc  
 cgcgtcatcctcggaagggtggccaacggctgcgcgaaatcgagcgtgttactgcgacgcgcacatcaacatcccagccagag  
 cgatgagagcgagttatcacgattgccggaaccaaggagggtattgccaggccgagcagagatccgtcagctgtcagccg  
 agcagtacaagaagtcacggaccgcacacgggtgccaaagttaccatccctcatcgtgggcccctacagcgagaacataaa  
 35 taagctgcaggaggagaccggcgttaggatcaacgtccgcgcgagcaggttcagaaggacgagatcgtcatctcgggcgag  
 aaggacgcggctgcagcggcaaggccaaagggtggaggccattacaaggatatgaaaagaagtgtctaccgtcagtgtagga  
 gtagctaaagccaagcaccgatattgctggcgaagggtccaccatcgccgagattctgagttgaccggtgtgtctgttag  
 agatgcctcccaatgactccccctcgagacgatcactttgctggggccgaagtggctttggaaatgccctaaccgttgtctac  
 caaaagtccaactcggcgaagtctgtggagatcaatcgccgacattggatccacaagtatgtgttcggtcgcaagggggccaaca  
 40 tgaagcagctggaggaggactgccccaacgtgaacgtgaattgctggaagacaagatcaagctggaggggagatcccgagaa  
 cgttgacagggtgtgacctactgtccgaaatcatcaaaaactacgaggagaacttcacattcgaggtgatgacgttaaccttc  
 gtactacaagcacatcatcgtaaggctggagccaacgtaaatgcctgaaggatgaactgaaggttaacattaacatcgaaagag  
 cgcgagggccagaacaacatccgatcaggggtcccaaggaggagtagcggcagcgacgttgtaattacaagaaaaatcg  
 acaactggaaaacgaaaaatgaaggatgtgatcatcgaccgctctcatcgttctattatcgagctaaaggcgagaagatt  
 45 cgcgaggtgaaggaccgtaccgccaggttacaatcacgatacctacgccccaggagaataccgatattgtgaagctgcgcgg  
 acccaaggaggatgtggacaagtgtcacaaggatctgttaagctggcgaaggagattcaggaatcgtcgacattatcgaggtg  
 cccatcttaagcagttccacaagttcgttattggcaaggcgccgctaacaatcaaaaagatccgcatgagaccagactaaaat  
 tgatctgcctccgagggtgacaccaacgaagtatcgaatcaccggcaagaaggagaacgtgctcgaggcgaaggaaacgta

tccaaaagattcaaaacgagctttccgacattgtcaccgaggagggtgcaaatcccgcccaagtactacaactcaatcatcggcact  
 ggccggcaaacatctcctcgatcatggaggaatcggggtgtttctatcaagttcccaacagcgactccaagagcgataaggt  
 cactattcgcgggtccaaggacgatgtggagaaggctaagggttcagctattggagctggccaacgaacggcagctggtctctt  
 accgccgagggtgcgcgccaagcagcaacaccacaagttcctgatcggcaagaatggcgcttctatccgtaagattcgcatgcc  
 5 actgggtgcccgcattatcttcccttcaaacgaggacactgacaaggaaagtgtaccatcattggcaaggaaagcgtaaaga  
 agggccgtgagcagctggaggcgatcatcaaggagtgcgacgaagtaaccgaagggtgaggtttctgtcgtatcccaagcaccac  
 aagcacttcgtggccaagcgtggcttcatcctgcaccgcatttcggaggagtgcgccggcggtgatgatctccttccccgtgctgg  
 catcaactccgataaggtgacgatcaagggtgccaaggactgcattgaagcgcccgccagcgcatcgaggagatcgctggc  
 atctggaagcgagaccaccatcgagggtggtgattccacagcgatcatcgcaccatcatggcgccacgtgatttaagggttca  
 10 acaagtcacctttgagttcgtgtgcagatcaagttccctgatcgtgatgccaccgaacccgtcgagggtctgaccaacggaggc  
 agcggagagaatggaggcgagaatgaaggccaggaggagcaggaagtagagaagggaagccgaacaggagccgggttc  
 gtcagtgcgatgttatccgaatcacgggcagaattgagaagtgcgaggccgccaaacaggctctgcttgatcttccccatcgag  
 gaggagttgtcgggtgcctttcgacciccatcgtaccatcatcgaccgcggtgccaatgtgcgtcagttatccaagcacgat  
 gtgcacgtagagctgccacctagtgagcttaagtcggatgtgatcaagggtcgtcggtacgcccgtcgcgtcgccgaggcccg  
 15 gaagcgtggtgaaaatgattgaggattacgagcgtgataggccgatcgtgagctgcgctcctttgttctccaggtggacgtaga  
 tacggaattccattcgaagctcattgtcgtcatggcgctgtgattacaagctgcgtgcccgtacacgacgtcatcttctgcct  
 aagcgggatgaaccaatgacgcacatctctatcacggctaccaggccaatgcggaggcagcccgcatgcccacctaga  
 gattgttggcgaccccgagacacttcacgcgaggttatcgatcgataaacgcatccaccccccacctcattggccaacgccga  
 20 cgcaccattcgaagatcatcgaggataataagggtgaacatcaagttctcagctgatgatgacaaccccaattcgatcttcatagt  
 ggcaagatagaggacgttgagaacgtcaaggagttgctcttcggcatggtgaggactacgagcgtgactacttgataacgtg  
 gcgatagcggccgaacgattggtgccttctaactgggttcttgatccgatccgcaggtgccagcgagaacggattcgtcatc  
 aaagacgcaccggtgggagaagcaaaagcaggccaaaaactgactgcgccaacactcagtcgaggaggacttcccgcact  
 tcgctgctggcgggggtccgggtgacctcacgcctatcacctccgtgtggggcccaaaaactaagtgcacggccgagtgctc  
 25 ccgatcgccagcagtagcagcaatactacaagtcggggtgcggcggggatcgagctggagatggaccaggagctggagca  
 gaagctggaactggaactgaattggattatcgggcaatgagcggcagagcagcggcagtcgtgcggacatctcttag

**Drosophila Gene Hit** BLASTN with rescue sequence 1: dodeca-satellite protein 1 (DDP-1) (AJ238847). TBLASTN with ORF2:dodeca-satellite protein 1 (DDP-1) (AJ238847).  
 30 **Drosophila EST** GH20785 (AI389573), LP07358 (AI294065)

**Annotated Drosophila genome genomic segment** AE003799

35 **Annotated Drosophila genome Complete gene candidate** CG5170 - Dpi dodecasatellite DNA binding protein  
 CG5576 - Bg5 involved in cytoskeleton organization and biogenesis which is putatively a component of the plasma membrane  
 40

**Human homologue of Complete gene candidate** CG5170- 4885409  
 ref|NP\_005327.1|pHDLBP| high density lipoprotein binding protein  
 45 >gi|2498434|sp|Q00341|HB

5

CG5576- 2e-07 4506539  
ref[NP\_003795.1|pRIP|  
UNKNOWN >gi|3426027  
(U50062) RIP protein kinase  
[Homo sapiens]

10

**Putative function** CG5170: DNA binding protein (homology with Scp160p, a new  
yeast protein associated with the nuclear membrane and the  
endoplasmic reticulum, is necessary for maintenance of exact  
ploidy)  
CG5576: death domain containing protein, possibly involved in  
signal transduction

15

20

**Confirmation by RNAi** CG5170: Reduced G1 and G2/M peaks indicating fewer  
cycling cells and more polyploidy  
CG5576: Loss of G1 peak

**Example 63 (Category 5)**

**Line ID** 40/2  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
5 **Map Position** 39B

**Rescue ID** BamH1

**Rescue Sequence 1**

TTTTGCCTCCGCTTTTAAATTAAAAAAATGTNTGTTTNGCCCTGGAGCTCTCG  
10 GTCTGTTAGCGAGCGTTGCCACCTTTCTGCGAGCTGTTGCTGCACACTGCCACT  
TTACGAACACAGCTCTGATAGCGGGACAAAATACGTCAAGGCAGCGACGGTG  
GGTTACTAGTGAATTTGGAACGGTGGTCTTAAGACGTACTGGTCTTTTATATTT  
TCATTATTTTTAAATTGTCGCTCATTTACCAATAAACCTTTTACTTTTTCTTG  
ATAGTCCGAAGTCAGATCAAATAGGAAGTTTCACAAAAAATTTTCATCCAGAG  
15 AAAATACGCCGACGCTATTCGAGTTTTTTGTATTTCGTTAACCGGGAAAGAATA  
GTTTCGAATTCGTTGCGACTTTATCGATAGTAGATTGCTATTATGGAGCCCACTA  
GTAAATTAATTAATTCAGACTGATAAAAGCGATCAACTTTTGTTAATGGGT  
TTAANTCTATAATAATNCTTAGTCCAAATTGTNTCAAAGTAGTCGATAATTTAT  
AATAACAGTTTTAGATGACCTCTAGGAAATAACTAATTACCCACATNCTTCAA  
20 GAAAGTGTNNCAATTTGTNCTATAATTAATAACAGTTGTATTAAATTATGTTG  
TNATTGTNACTCATAATACAAATTAACAATATAAACACACATAAATAAGAG  
AATTGGAATATTTGTCTCAGATTAGATTTNCCAC

**Rescue ID** EcoR1

25 **Rescue Sequence 2**

AACGGGGGGGCTTCCGCGNCNCCAAAACGCAATNTACCGTTCATGCTGTGAAG  
CGAAAAAGAGTGGTAGCGCCTACCNTGGCATATGTAGTTAAATCCGTGAAAT  
AAGTGAATAAGAATATATGTATGTACTTAATTCGAAAACCTTTTCGCCGTCAG  
CACAACGGGTGAACGAGAGAGCGGAAGTGGAGTTTTTTGTGGCGGGTCGTCT  
30 CGCTCGCACC GCAAANGTCGTCCGTGGCTGCGTGTATGGGTGTGTGGA AAAA  
GCGTCGAGGTGAATGTGGATTTCTAACCACACCAGCATTGCAAAGACATTGAT  
TGATATTTAAAGCTGCAGCAGCGAACAAGCAAATCCTAATTTTCGGCAAAGTT  
TAAGAATAACGAGTGAAGTGGGCGCGCGCAATAAGATAAAATTGAAGGTTAT  
CTGTGTGCGTGTGAGTGACCGTNTACCAGTGTGTGTGTGCGANCGTCCATTGT  
35 AAACAAAAACAAGTGTGTGAGCGGAGAGAAGAAAGGGAAAGAGAGAAAAG  
AGCGAACAGACTGGCGAGAGAAAAAAGAGATGCCACAAANAAGCAGCGCA  
CAAAGGAAAGCTGAAAATTTCAATAAATCTGCAAAAGTGAAGAAAACCAAA  
GAACCCGCAGTCNTGTAAATAAAACCCAGANTCCAAGAAACNTTAAAGAA  
GCAGTGCAAAACAACTGGTGCTNTGAATGCGGTTTATTTGAAAAAAAATGCA  
40 ATTCGGTCCGATGGAA

**Genomic hit, Accession No.** CSC:AC014744

45 **Drosophila EST** several including LD46342 (AI544109 BLASTN similar to mRNA  
L07550)

186

Annotated *Drosophila* genome genomic segment AE003669  
Annotated *Drosophila* genome Complete gene candidate CG8678 - novel with ankyrin  
homology

5

Human homologue of Complete gene candidate CG8678 -gi7661580  
B69CEC399B56F35C  
[ref]NP\_056425.1|DKFZP434J  
154 protein [Homo sapiens]  
(2.20E-85)

10

**Putative function** Novel protein with ankyrin domains, unknown function

**Confirmation by RNAi** Reduced G1 and G2/M indicating fewer cycling cells

15

**Example 64 (Category 5)**

**Line ID** 55/12  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** NR  
**Map Position** 49C

**Rescue ID** BamH1

**Rescue Sequence**

10 TCTCATGNTCAGGGGGCCTTTACNATGTCAAAGAGCAAATTGTCCACAGGGCA  
 GCAACCGCAAGTGAGAGACGGGTGGAAAAC TGGGCGGCATGACCATGAATGA  
 AAGCCGCGACCGGCAAACGTGGCCCGCCACAAAGCGAGCATT TTCACATTTT  
 AACTGTCTGGACATTTTGTAAAGTTACACCAAGGCAATGATACCAGTAAAAAAG  
 AAGAAACAATCATTTTGAATAGATTAATCACCTGATTAATGTTGGTTGTATGT  
 15 TGATTGTAGGTGTTTTAATATACAATGTCTCTATTACTGCTTTCCTTTATTCAA  
 AGCCATGTGTAAGTGTAAGTTCTCGATTTCGGCTAGATTTTGAAGTTCTGCCAT  
 TATCAATTAAAAGTCCAGTTCCTCTATAAATTGGTAATAAAATAGCTCTTTACA  
 GCCAAGTATATGTGCAATTTTGTAAAGATTAAANGTCCAAATGTTGTGAACCTT  
 TCCTGGCCCTGAATTTTAAAAAACCATTAAATTGGTCCCATTGACATTAAATG  
 20 TTCTATGTACATTAATATGACTTTTGTGGATGGTTTTATAACAAGCATTACT  
 ATATTCTAAAAATCAAGGATAAAGGACNAGCTTTACAGGAGGTAACATTCCTA  
 TTGTACGGCTTTATTTTCTTATACCCATAAGAGCATACCACTAGGATCCGTCGA  
 CCTGCAGATCTCTAAAAACTTGCCTTTGCTGGCGTTTTCCATAA

25 **Genomic hit, Accession No.** AC007085

**Associated ORF**

Genscan ORF1 predicted sequences >21:54:11|GENSCAN\_predicted\_peptide\_3|108\_aa  
 MGLVTAAFKLKRKDIQDRYQHDINRICHTRSTAHTAYAHFAEHLRRSPRQRFVN  
 30 GKGAALVLILLVSAARQFSGSTGAYKLGNRVGVKVEGEQQEYKLQDRTTTHFCGN

>21:54:11|GENSCAN\_predicted\_CDS\_3|327\_bp

atggggctggttaaccgccgcttcaagctgaagcgcaaggatatccaggacagatatcagcatgatattaaccgcatctgccaca  
 cacgtagcacggcacacacggcgatgctcatttgcggagcatctgtgcgacgaagtccacgtcaacggttgtcaacggcaa  
 35 aggtgctgcgcttgctcatctctctgttctgcggctcgacaatttctggctcgacaggtgcctacaaactgggtaataagagttg  
 gaaaagtagaaggggaacagcaggaatacaaaactacaagacagaacaacacattttgtggcaattaa

Corresponds to CG8732

40 **Annotated *Drosophila* genome genomic segment** AE003836  
**Annotated *Drosophila* genome Complete gene candidate** CG8732 - l(2)44Dea  
 homology to fatty-acid-  
 Coenzyme A ligase, long-  
 chain previously described  
 45 spindle/chromosome



abnormalities in neuroblast  
squashes

- 5     **Human homologue of Complete gene candidate**     1e-171 4758330  
ref|NP\_004448.1|pFACL3|  
fatty-acid-Coenzyme A ligase,  
long-chain 3  
10     >gi|4165018|dbj|BAA371 and  
LCFD\_HUMAN LONG-  
CHAIN-FATTY-ACID--COA  
LIGASE 4 1e-157
- Putative function     Fatty acid CoA ligase
- 15     **Confirmation by RNAi**     Only wild type profiles observed

**Example 65 (Category 5)**

**Line ID** 6/7  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** NR  
**Map Position** 28E

**Rescue ID** BamH1

**Rescue Sequence 1**

10 TATNAATAATCATAGGGCTCTTGCTCTTACGTGTAAGGCCTGCCCCCTCTNCCA  
GTCTATATACAAAGAAAAACACACACACACTGGCACACTGGTGTTCGCATATG  
CCAAAGCCGAGTTAATTTCACTTTGTTAATCTATCGTTTGGTGTGTTTGCATTT  
TTTAACCGCGCAAACGGTATTTGCGCGTTTGGCGCCTCTTACTTTGCGATTTAT  
TGCACCGCTTGGCTGTGTTTGGCAATTTCTATCTTGATTTTCATTGGTATTCACG  
15 CGTAATGTAATTTCTTAGCAGCGTGACCGCGCCGATAACGATAAAAAATACCAC  
GGGACCAAAAATAAATACCATATGATACCACTTCAGGGAAAAGAAATCCTAT  
TTAATACCACTCACTTTAAAAATAAGTTTTTAAAAATATATATNTTTATTTAAA  
AAAAGGTGTATTTATAATCAAATACTCGGTACTTNTTAATTACTCCAAGAANA  
ATTAATTTGAAAAAAGGGGTTCATTATAAAATATATATTAACCGCTTACAC  
20 ATAATCCCCAAACAAAACAGCGATTGGGATTTAAAAGGTTCTAAGTCCATCAT  
TATAAAAGATCATTTCCGAAAAACAAAAGAAATAGATTCAAAATTAGGCGAC  
ATCAGCCCGCTGATAANGATCATAAAAATACAGAAAGCTNATTCAGCGAATCA  
GAAANTCCTACTCGCCACTATCCGAAAACNTNGAAAAAAAATGG

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

TGAAAGGTAGCAACAACGTTTCCTTGGA AAAAGCTGTAAATAGTAAACAAAA  
TTGTCAAGTTAACGAGCCAAAGTTATTAATAAGGTTGAGTACGTTGGCATC  
GGCTGCCCAGGCAGCAAANAAAAACAAAGACGCAGTTCAAGATCAGCTGGAC  
30 ACTTAGAAGANTTTAAGAATTGAAGCACATTNNAAAGAAGANAAACAAGAAC  
CCCACCAAAAACCCGCGTGCGTTTGTATGTGTGTGCCATCAAATTTCCCGC  
ACTGGGTGAATGTGCNTGCGTGTGTNTGTGTGCATTTAATTTTCTACCAATAA  
TCGCCTTCCAAGAAGTGAATACCAGCCGATCCACCGCTAAATCGAAAAAAGTT  
TNACTCTGGGTAAANTCACTGTTTACGGCTTTTGTGCTATAATTACCTTTCCCG  
35 TAAGCNGTGGGAANCTAAAANCCAAAACNTNAGAATCCGAATTCCG

**Genomic hit, Accession No.** CSC:AC017934

**Associated ORF**

40 Genscan partial ORF1 predicted sequences  
>22:35:21|GENSCAN\_predicted\_peptide\_4|128\_aa  
MGTNSGATAGINNKPVGATGAGVLVGGGVGGANSSIGGVLSNSLGGGGSGGLS  
ISGLNAGGQNAVGGMGNVGGDDGGNGMVGGGVNNQQATTPQYTIPGILHFIQ  
HEWSRFELERSQWDVDRAELQ  
45 >22:35:21|GENSCAN\_predicted\_CDS\_4|384\_bp

190

atgggcaccaattcgggagccaccgctggcataaacaagaacgggtggcggtgcaacaggagccggcgctctttaggcg  
 gcggtgtggcggtgccaattcctcgatcgcggtgtcctgtcgaacagcctggcggtggcgagcgcggtctgagcatc  
 agcggcctcaacgctgggtggacagaaacgccaatgtggcggaatgggcaacgttggcgcgacgacggcgaaacgggatg  
 gtggcgcggtgtaaataaccagcaggccacaacgccccatacacaataccgggcattctgcacttcatccagcacgagtg  
 5 tcgcgttcgagctggagcgatcacagtgggacgtggacagggccgaattgcag

**Human Homologue** TBLASTN with ORF1: very weak homology with striatin,  
 calmodulin-binding protein (STRN) (NM\_003162.1)

**Drosophila EST** several including LD42534 (AI516610), LD03224

**Annotated Drosophila genome genomic segment** AE003619

**Annotated Drosophila genome Complete gene candidate** CG7392 – novel WD40 family  
 member

15 **Human homologue of Complete gene candidate** CG7392- SG2N\_HUMAN  
 CELL-CYCLE NUCLEAR  
 AUTOANTIGEN SG2NA  
 (S/G2 ... 622 e-178 A cell-  
 cycle nuclear autoantigen  
 20 containing WD-40 motifs  
 expressed mainly in S  
 and G2 phase cells

25 **Putative function** WD40 protein a novel nuclear protein mainly expressed in S and  
 G2 phase cells that was characterized using autoantibodies from a  
 cancer patient

**Confirmation by RNAi** Reduction of G1 peak , more polyploidy

30

**Line ID** 103/1

**Category** 2nd chromosome, small imaginal discs

35 **Reversion** R

**Map Position** 57B

**Rescue ID** BamH1

**Rescue Sequence 1**

40 GATTTCAAAATTAGGCGACATCAGCCCGCTGATAAAGAATCATAAAAAATACT  
 GAGGCTTATTTTAGCGAGTCAGAGACTCCTACTCGCCAACATATCGAAAACATA  
 GNGAAGATATAGTCGCCAACCGATCTGCCTTCTATAGTGTTGCTTATTGTTGTC  
 CCCTAATCAAATTAATAAAAAATCTGCATTAGGCTGCTTCGCCGGCCAGCAACA  
 AATGTTTACACCTACTGTACTTTTCGCAGAACAGAGATCCAAATGCAGGATC  
 45 GTTTCATGACTGTACATTTATTTCGGATTAGACATTAAATTACACCCTACAGCT  
 ATACATACTAACAGTGAACACGGCAAATGCTTAGCTAGCATTGGGCCACTTTC  
 GTTGACTGCGAATAAAAAATGATTGGCCGATGCCTTTAGCAGATTCTTTTGAT  
 CGAATTACTCGGATGGCTTGTGTGTCCACCTCTTACAAGAACTCCTCGCACCA

ATCGTTGAGACAGTTGTAGCAATCGGATGCTTGGTTGGAGCTGGCGTGGCACA  
CCTTCTTCATCCAGTCCCTTGGACAGNTTCTTGGNCCTTTTCAGNANCAGGATCT  
GGTCCCAAACGGNGGAAGGCCTAAAACGAATGGNAATTGATCGGTAGCCCTT  
GACTGGCATTGGTAATTTGCGCACATGGGNGTCATCGGATTTACACACGCACC  
5 ATATCGAATCAGCGTCCTTAAGCGTCAACCGAGGGTTTCCCCAATTCCGGCCA  
GTTCCGTCACCGACTTGGTTGCCATTGG

**Rescue ID** EcoR1**Rescue Sequence 2**

10 ATCAAAGCGNCTGGGCCCCGTGCATCGCCNCAGCGTTCGTCTTAATTAATTAGT  
GATTGCAAGCGGGTGCAATTATGCACAAAATTACGGACTAATACAACGCCC  
GCTTCGCGCTCTCTCCATCTCCCTTCCAAATAGTCGTTTGCTCTTCGCACACAA  
AAGTGTAACCCCTGTGAAAGGTAGCAACAACGTTTCCTTGGAAAAAGCTGTA  
AATAGTAAACAAAATTGTCAAGTTAACGAGCCAAAGTTATTAATAAGGTTTCG  
15 AGTACGTTGGCATCGGCTGCCCAGGCAGCAAAGAAAAACAAAGACGCAGTTC  
AAGATTCAGCTGGACACTTAGAAGAGTTTAAGAATTGAAGCACATAAAAAAG  
AAGAGAAACAAGAACCCACCAAAAACCCGCCGTGCGTTTGTATGTGTGTG  
TGCCATTCAAATTTCCCTGCACTGGGTGAGTGTGCGTGCGTGTGTGTGTGTGTC  
AGTTTAATTTTCTACCAATAATCGCCTTTCCAAGACGTGATTACCAGCCGATC  
20 CACCGCTTAAAATTGATAAACGTTTTAACTCTTGCGTTACATCAGCTGTTTTAC  
GGCTTTTGTGCTATAAGTTACGCTTTTCCCGTAAGCCGTTGGCAACACTAGAA  
CGCAAAAGAGCATAAAGAATCGCGAGTACCGTANAGAGGAAGAGAGGAAGA  
GAGAGAGATAGAGAGTGTGAGCGTGTGAGTGAGCGGGGAATGTGGGGGCGGT  
TCCGGTGCGAAAAAACGTAGTAGTAGTACATNNAGAGAGTGCGAACGAGAGG  
25 GAGGCAGCCAGCGAGTGTCTGCGACTGCTCCCCCTTTACCCTCGTCGCTTTT  
CTATTCGGAAAAATTCAATGACCTCATTTGTTTCATGTGCCGAACTTTGCTTTTC  
TTTCCCAACCTAAAAACGCAAAAAAAAAAAAAACNCCAAACAGGATATACGTNG  
GAACANTGANCAACNANTTCGANAAAACCAACAACNANGGACCGTGCCCTG  
GGGCNCCTGAAAGGCAAACAGCTGGCNCNCAATCCGGAAGAGGATCNGGAA  
30 NAACAGGATCNGCGGGCNCAAGGATCNCCGGAACAGGCAAAGGAAACNCCC  
GGCNCACNGCACAAGCCNCTGAAAAGCAACNTGAACCAATGGGCACCANTTC  
CGGGANCCACCGCTGGCATTAAA

**Genomic hit, Accession No.** CSC:AC017934

35

rest of results as for line 6/7

**Example 66 (Category 5)**

Line ID 65/24  
Category 2nd chromosome, small imaginal discs  
5 Reversion NR  
Map Position 48A

Rescue ID BamH1

**Rescue Sequence**

10 TACGATTTTTGCANTGCNCCATTTTCGTGGCACCCGATTTGTATATATATTTTT  
ATATAACCCACGGATTGCCAACTTTCATTGCCCTTTCACACTCTTATTCGCCAT  
TTATGAACTCTTCTTTGACGATTGGAACGGTTCCTTTTCGCTATTTTCGACTGC  
ACCCGCGCTCTTTTCGCTTCGCTCTCCTCCCTCTCTACACACCGCTCTTTATCCT  
TAATTGCTTTTTCTATTTAGCGGAATTGATCGTTCTCAACTTGGTCGCCATTGC  
15 AGCTCCACAGGCGAAAAAATCGGTGGAAATGCCAATACAGGTGCACGGCGAG  
TGCCGATAAGCTGGAAAATCGGGAAAACGCACGCCTACACATTCATTGCCAG  
CATCGGCTTTGCCTTTTCGCTGTCGAGATTAGCATATTTCCACTTTTGGTTCGC  
GCACAACACTANCTAAATTATTGNTATTTTTTTCCCAACTGTGAGGTGAAAC  
TGTGAAACAAAACCACTGTGGGCGGGTCAGTGTGACCCTCTCGCGGTGGGTG  
20 AAAATCCTAGTGAGCTTCGTTGTTAGGGCTGTATGACACGAAAGCAAGTTGAA  
AAGAACTTTTTTAAAATTATTTGGTTAATTGAGCAGAACTAAACTATATN  
AAAATATTTAAGAATNCAGATTAGTGATGTATTTAATATAATAATAGTAAGAT  
GTTT

25 Rescue ID EcoR1

**Rescue Sequence 2**

CTTNTTTGATAGANATAGGCTTCTTTTAAAAAANAAGCAGCANCAGGGG  
CCCNAAAGTGCGTGNNTGTGAACGCTGATTGCTTGCAAGTGTGTTTCGTGTGTG  
TGTGATTGTGTGCTCCGANCAAGTGAAATCAATAATATTTGCAGCCACAAGCA  
30 ATTAATAAAAACTGCAATAATGTCAAAAAATCTAATTGAGGCAACAAATTAN  
CAAAGCCATNAAAGCAGGCTGCACTGCGAGAAAATTGTGCCTTTCCACAGAT  
CTTCTGCTGCAAGCNAAAGAANGTAAGCAAGTCGGCCANTTTATTNCATTCT  
TCTCATCTCTCTTCTTCGCGAATTGGCGCNTANCACTTACAATAATTNATATNA  
CTTCTTAAATTTCAAANTCCCTTTCNTGAACGGANCTTTTAACGGAAAACAAA  
35 GCGGGTAAACTAACTTAACTAACTAATTANAANTGTANGTATAAATGAACC  
GAACTCGCTTTAGATATNATGCGTTTCACTAACANATTANAACAACTTTGAA  
GCTGTANTGTCAGGTTGTTATTNCGTTACCANATGTAGACTGNCCGNNAATT  
TNACCTTTCCCATANTCTGTTCTTAANTGINTTGTTTTTTCCCAATNNTTTGATC  
ATNCNTTGGTNAATNANCTNAACGGCCCAAAGTNAATGAATTCCANTCACGTC  
40 CACTGGCTCTGGTTCNATANTTAATNGGCTGTTTCTTACTTCCCTTAACCCTAA  
CATCTNTTAATCACCTGTGCCATNTGTTTGTGTGTGTGTGAACGAATGAGAAA  
AAAAA

Annotated *Drosophila* genome genomic segment

AE003825

**Annotated *Drosophila* genome Complete gene candidate** CG9005 - novel putative cell adhesion

5 **Human homologue of Complete gene candidate** CG9005- Ensembl predicted gene  
ENSP00000006008  
Gene:ENSG00000005238  
Clone:AC004472  
Contig:AC004472.00001 6.00E-38  
10 (KIAA1539 protein AB040972) and  
AK022837 Homo sapiens cDNA  
FLJ12775 4e-33

15 **Putative function** Putative cell adhesion protein

**Confirmation by RNAi** Reduced G2/M peak

**Example 67 (Category 5)**

	<b>Line ID</b>	74/3
	<b>Category</b>	2nd chromosome, small imaginal discs
5	<b>Reversion</b>	NR
	<b>Map Position</b>	47A
	<b>Rescue ID</b>	EcoR1
	<b>Rescue Sequence</b>	
10	GCACAGAATGGCNCCTTCACGACAAAAGATCTNCNAATTAGGATGATGCAGA AGGAGGACACGCTTTTCATTATCTGGTTGCCACCTAATTTAAGTTCCACATCAA GGGAAGAAGGAAATACGTTCCAACGGACGTCAAATTTACTAACTACACTACTT GAAAAGCCTGTCTATAAAAACACGATAACGTTTTTGCTAATCTCAAGACAATG TTAAATATAATTGGAGAAAGTATTGAATATGAATATCACAAAAATTGTTTAGG GTCTCTACGTGGTAAATAGTATTTGGCATAGACAGTGAGATGTGAGTCGTACG TACTAATTAATAAAAGTTGTTCAARAGAACCTCATATACTGTAAGTGACAACGA ACGAAGCTGACAACTCTGCTTGACATATTTGGCGGAGTTTCGAAAATATCATC GCATTGGTATTGTTTTGTNTCCACCNTGGGGCGAGATTTTGTGTGTGCTTTAC TTTGCTTGTTTTTCNCCACAAANCGAACCATAATGTTTCGAAATGGTAAAATTA CCGTGCCAACAAAGCTCTCTCTCTCCCACTCCGAACTCTCTCATCTCTCCTTG CAATTGTTTAAGGTGTGCAAGGAAATGAAAAATGTCCCGGCTGTGTINCCATG CATTCCCTTCAAAGCCAATTATNTTTGTGCCTCTCCAACNTTTTTGATCGGNN TGATTTTTTTGGCTCCCNANTCCCCCCCCCTTCNCCCATTCCGGGTTANAT TATTNTNCCAATTTTCCTATTTTACGGTCCCNGTCCCTGGAAATANTTCCTNC AATCNC CGCTCCATNTCNCCATNTTTGACAGATTTTC	
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003829
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG12052 lola -a specific RNA polymerase II transcription factor involved in axon guidance
30		
	<b>Human homologue of Complete gene candidate</b>	1e-09 3789797 (AF059569) actin binding protein MAYVEN [Homo sapiens]
35		
	<b>Putative function</b>	lola-like specific RNA polymerase II transcription factor
40	<b>Confirmation by RNAi</b>	Almost no G1 peak and increase in G2/M peak indicating arrest in G2/M

**Example 68 (Category 5)**

**Line ID** 79/7  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** R  
**Map Position** 55B

**Rescue ID** BamHI

**Rescue Sequence 1**

10 GTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGTGTGC  
GAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCCTCCGGGGTTAT  
CGGTAGCTTCTTCTAGGCTGAGTGCATTTTCGTTGAATCGTGGATGTTGAAAGTT  
GTCTAATTTCCGAACATTGATTTTTCCCTTCCCGTCAAGAACTGCATTGT  
TGCTTCTTGAAGACCAGTTTTGGTAACATCAGGAGAATGGAAAGGAGCGAGT  
15 GAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACAACA  
ACAACAACGGTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAACAATT  
TGAGCAGCTCCGTTTGTGTTATTGCATTACTCAATCGGGAAGACTCTACACTC  
GACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCTTCCTTTGTTT  
TTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGAACCAC  
20 CAAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAATATTATT  
GTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTTCATATAC  
ACGCAGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCCGTN  
CACATACACTTGTCTTTTTNCCACACACTTTCCTAATCAT

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

NGNGTCTCATGCACCCTGGCCCTNAGCTGCATAAGTGTAAGTGTGTGNCTGT  
GTGCGAGTGTGGGTAGGCGGCGGCAACTATCTCGCTTGCTCTTGCCTCCGGGG  
TTATCGGTAGCTTCTTCTAGGCTGAGTGCATTTTCGTTGAATCGTGGATGTTGAA  
30 AGTTGTCTAATTTCCGAACATTGATTTTTCCCTTCCCGTCAAGAACTGCA  
TTGTTGCTTCTTGAAGACCAGTTTTGGTAACATCAGGAGAATGGAAAGGAGCG  
AGTGAGTCGGTGAGTAAGTGAGTGAGCGATGCGAGCGACAAAATCAACAACA  
ACAACAACAACGGTTCAAAACGAGTTCCAACGAAAGTTGCAACACTCTCAAC  
AATTTGAGCAGCTCCGTTTGTGTTATTGCATTACTCAATCGGGAAGAACTCTA  
35 CACTCGACGGAATAGTGTGCTCGTCTGAAATTTATCNATTTCCATTCTTCCTT  
TGTTTTTGGGCCAAACAATGGCNTCGGCAANCGTTCGTGGAAAACCGCAGGA  
ACCACCAAAATGCCTGGCGTCACATTAACCGAGCCGCCTTTGTTTATGCAAAT  
ATTATTGTAATATTTGGTNAAAATTAAGTCGCGCTTCNCGTTACTTTTTATTTTC  
ATATACACGCAGCAGCACGCATACAGTCACGTCACGCACACATACAATCGCC  
40 GTNCACATACACTTGTCTTTTTNCCACACACTTTCCTAATCATNNTA

**Genomic hit, Accession No.** AC004296

**Associated ORF**

45 Genscan: ORF2 predicted sequences >15:31:31|GENSCAN\_predicted\_peptide\_3|109\_aa  
MVTSEFRHLRDEKSFTDVTLACEGQTCKAHKMLVLSACSPYFKALLEENPSKHPHIL



KDVSYIHLQAILEFM YAGEVNV SQEQLPAFLKTADRLKVKGLAETPSSIKREG

>15:31:31|GENSCAN\_predicted\_CDS\_3|330\_bp

atggtgacctcggtccgtcacctgcgcgacgagaagagcttcacagatgaacactcgctgcgaggccaaacctgcaaagcc  
 5 caaaaatgggtgcttccgcttcagtcctactttaagcgctactggaggagaacccatcgaagcatccgatcattatcctgaaa  
 gatgtctctacattcacctacaggctatactggagttcatgtacgccggtaggtgaacgtgtccaggaacaattgccagcatt  
 cttagaccgccgatcgctcaaagtgaaggcctcgagagacaccagttcgataaagcgggaaggttga

10 **Drosophila Gene Hit** TBLASTN with ORF2: several zinc finger proteins including  
 Broad-Complex mRNA for BRcore-Z2 protein ( X54665)  
**Human Homologue** TBLASTN with ORF2: kelch (*Drosophila*)-like 2 (Mayven actin  
 binding protein) (KLHL2) (AF059569)

15 **Annotated Drosophila genome genomic segment** AE003800  
**Annotated Drosophila genome Complete gene candidate** CG5738- lola, lola-like  
 putative kelch-like putative  
 specific RNA polymerase II  
 transcription factor known to  
 affect disc morphology

20 or could be CG10914 - novel  
 unknown

25 **Human homologue of Complete gene candidate** CG5738- 9e-09 3789797  
 (AF059569) actin binding  
 protein MAYVEN [Homo  
 sapiens]

30 CG10914- predicted gene  
 ENSP00000051207  
 Gene:ENSG00000047313  
 Clone:AC068261  
 Contig:AC068261.00019  
 4.00E-49 (potential cell  
 35 division GTP binding protein  
 1: ENST00000051207

**Putative function** CG5738: lola like specific RNA polymersae II transcription factor,  
 CG10914: Possible GTP binding protein

40 **Confirmation by RNAi** Both show marked reduction in G1 to G2/M ratio

**Example 69 (Category 5)**

**Line ID** 80/2, 81/8  
**Category** 2nd chromosome, small imaginal discs  
**Reversion** R  
**Map Position** 57D/E

**Rescue ID** BamH1

**Rescue Sequence 1**

10 CANTTTCAGAGGCCATAGNCCTTCACAAAATTCNCCATCTCTGCCCCGGCATCC  
 GTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCACTCGATGGTC  
 TGCAAAATTGCACATTTATTAGATTTAATAAAATTTTCAACTGTCCGCGANCAC  
 GTTTGCTCGTGTTGAATTTTCGAGTACAAAATTAGTGCGACTGTTGGATTGCATT  
 GAAATGCCAAAAATCGGTGTGACCATTTCGAAGTCCCCACAGGCTCATGACTT  
 15 TCGCGGTTACCAAATCCAAATAACGCAAGCTGGTCACGCTGTCAAACATCGG  
 TGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTTCTTGCGGCCGT  
 AAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACGTAATTGGAACA  
 AATGTTTGCTGAACCACAACCGCCCACTAAATGTTANCCGCCAAGTCTTTTCC  
 CCCGCCGCCCGTCNTCNCNTCNCNCCGATTATTTGGTTTACAATTTGCTTAC  
 20 ACAAGTGCAATCGTCGATAGCGCTTCATTTGGAGTAACAAGTAATATTTTGC  
 GCCGTAAGTGTGTCGCGGTATCAGACAGAAGGTTGGTATCAGTTCGACGCAG  
 CTTGTGACGGTATTGCATACGCGGCGAAACGCCACGTGAAAACGGATCGCA  
 GTTCTCGAAAACCTCNGGATAAAAA

25 **Rescue ID** EcoR1

**Rescue Sequence 2**

TGGGGTCTCANGCCCCGACGGCCATATTTTAAACACAAGATTCNNCANCTCTGC  
 AGGGCATCCGTGCTTGAAAATGGTGCCAATGCGTCGTGGAGAATCTGCTGCAC  
 TCGATGGTCTGCAAAATTGCACATTTATTAGATTTAATAAAATTTTCAACTGTC  
 30 CGCGAGCACGTTTGCTCGGTGTTGAATTTTCGAGTACAAAATTAGTGCGACTGT  
 TGGATTGCATTGAAATGCCAAAAATCGGTGTGACCATTTCGAAGTCCCCACAG  
 GCTCATGACTTTTCGCGGTTACCAAATCCAAATAACGCAAGCTGGTCACGCTG  
 TCAAACATCGGTGACGGAATGGTGACGACACAAACAATTTGCTTAAAAACTTT  
 CTTGCGGCCGTAAAAATGCGCAAGCAGCCTGGCAGCGCAACGCACGTACACG  
 35 TAATTGGAACAAATGTTTGCTGAACCACAACCGCCCACTAAATGTTAGCGCCA  
 ACTNCTTTTCCCCGCCGCCGCGGTCGTCNTCNCNCCGATTATTTTGTGTTACA  
 ATTTGCTTACACAAGTGCAATCGTCGATAGCGCTTCATTTTGGAGTAACAAGT  
 AGTATTTTGCGCCGTACTGCTGTTCCGCGTATCANACAGAAGGTTGGTATCAG  
 TTCGACGCAGCTTGTGACGGTATGCATACGCGGGGAAACGCCACGTGAAAAC  
 40 GGATCGCAGTNCTCGAAACTCNGGATAAAAAGAAAAAGTAGGCTGAATG

**Genomic hit, Accession No.** AC007175

**Associated ORF**

45 Genscan: ORF2 predicted sequences >16:09:09|GENSCAN\_predicted\_peptide\_3|2497\_aa  
 MNEGNSAGGGHEGLSPAPPAVPDRVTPHSTEISVAPANSTSTTVRAAGSVGAALP

ATRHHQHIAATQVKGIASSSSKQQKQLASAPVPLSPLPQQQQQTAEATAAAAAP  
 AHSNVSVSSSTIEASVLPQAKRQRLDDNEDRTSAASIVGPAESSNIVSSLLPASVA  
 SSSEVGGLSSTALQDLNALKKRILQQKLQILRNLKERHLENVSEYFYLQNGGSM  
 DYPAWRKKTPTPQFISYSNANRIDQLIHEDKPSTSAQAAAAAQNQKYTTQQTDSVE  
 5 SSLVSGIGTGATKAPLDGNISNSTVKTNTQSQVPSKIGSFTESTPAATESNSSTTVP  
 GTATSGAATSTSATSASGNVLAVEAEIKIPAVGATPVAISTKLPAAVVQLTQQG  
 GTPLPCNTSAGSTALRRPQGQNNASSGSAASGGGGSLTPTPLYTGNPAAALGG  
 SGGLTPGTPTSGSLLSPALGGSGTPNSAAQEFSEKAKQEVYVMQRISLQREGL  
 WTERRLPKLQEPSRPAHWDYLLEEMVWLAADFAQERKWKNAKKCAKMOV  
 10 QKYFQDKATAAQRAEKAQELQLKRVASFIAREVKSFWNSVEKLVEYKHQTKIEE  
 KRKQALDQHLSFIVDQTEKFSQQLVEGMNKSVAADTPSLNSSRLTSPKRESDDDFR  
 PESGSEDDEETIAKAEEDAADVKEEVTALAKESEMDFDLNDLPPGYLENRDKL  
 MKEEQSSAIKTETPDDSDDEFEAKEASDDDENTISKQEEAEQIDHKKEIDELEA  
 DNDLSVEQLLAKYKSEQPPSPKRRKLAPRDPELDSDDDSTAVDSTEESDAATED  
 15 EEDLSTVKTDTDMEEQDEQEDGLKSLMADADATSGAAGSGSTAGASGNKDDML  
 NDAAALAESLQPKGNTLSSTNVVTPVPFLLKHSREYQHIGLDWLVTMNERKLN  
 GILADEMGLGKTIQTIALLAHLACAKGNWGPFLIVVPSSVMLNWEMEFKKWCPG  
 FKILTYYGSKERKLKRVGWTKPNAFHVCITSYKLVVQDQQSFRRKKWKYLILD  
 EAQNIKNFKSQRWQLLNFSTERRLLLTGTPLQNDLMELWSLMHFLMPYVFSSHR  
 20 EFKEWFSNPMTGMIEGNMEYNETLITRLHKVIRPFLRLKKEVEKQMPKKYEHV  
 ITCRLSNRQRYLYEDFMSRAKTRETLQTGNLLSVINVLMLQRLKVCNHPNMFARP  
 TISPFQMDGITFHTPRLVCDIMEYDPFTQINLETNLNLLHLEQMTAYVSHKSRL  
 APPRKLIEDIDTAPLPAPRCPNGKYRFHVRSAELAQRILNNAVKVGASPAMRLE  
 GSKIMPMRNLPSGRVLKRVASINPVNMAKPVVINSVVTSSSTTASSPTGAL  
 25 SVLSNSKLLGARSQINAPTPAKVAKTMQDGKPPFYLTPTNSGAAGARLTLSKT  
 TASASTTTSRTTVTASTTSGQQLIRDPIVKDLATHVKSTVQKQSIANGKTEPEEETE  
 AEDPYKVQELIQMRKEQRLAALKRMAMINRRRTDATPIYGEDCREAIQRCMQAT  
 RSLKRSTWQTRGYANCCTAMAHNRGWSLNHLLKSFEERCADLKPVFANFVIYVP  
 SVCAPRIRRYVQNLSSSTHWQHEQRIENIVDQALRPKLALLHPIISEMTTKFPDRLI  
 30 QYDCGKLQTMDRLLRQLKVNHRVLIQTQMTKMLDVLEAFLNYHGHYLRDGS  
 TRVEQRQILMERFNGDKRIFCFILSTRSGGVGINLTGADTVIFYDSWDNPTMDAQA  
 QDRCHRIGQTRDVHIYRLVSERTIEVNILKKANQKRMLSDMAIEGGNFTTTYFKSS  
 TIKDLFTMEQSEQDESSQEKENKDRIVATTTLSDTPTSTVVETEKQSLRAFEHALA  
 AAEDQDVQATKTAKAEVAADLAEFDENIPIATEDPNAEGGPQVELSKADLEMQ  
 35 NLVKQLSPIERYAMRFVEETGAAWTAEQLRAAEALEAQAQREWEANRLAAMHK  
 EEELLKQETEAEEMLTYSRKDSSNQVNTKTDSSNSNKRRLVRENRRNSAQKLSRSV  
 SSHSTGSNNKNSKSATTRGNSQNSLNQTVPGSGISRVNRTGAGVSSSSRGKSNS  
 KSTGKGTDAAPQVRRQTRLHSLGAVNMAASARTPPTRKTTRTALAASAAASTLED  
 ASLIVEERPKRQSANIAMSKMMKTPFKQNVPSNISIKTTPPKRGRRDSVAAAATRS  
 40 KLLERRATIAAPLKHMDDESQDEEEQEEQSEEDTEGEEANATVDDDEEGEEEL  
 ASLDEETIQTGSQTNDEEDDDDEEVGEEGMVDIDTEDSEADVKSSTYGTADGK  
 PEEAESLDGWDADHDQVQDTTMTSSTYVNVSEESDTDEHHDSKAEAKEPPQNSDK  
 SDESEAVGHTPRTRSRGTVKINLWTLDVSPVANALNKSSANRSLKKAPRTESTPK  
 ESQSEPRRKITQPKLPKKEETNNKSNSNIGTLHRWISKSPRVMLRSTPVTAAASSS  
 45 AAVSGVSGGNASSSGTAR

>16:09:09|GENSCAN\_predicted\_CDS\_3|7494\_bp

atgaatgaaggaattcagcaggagggggcatgaagggtcagccggccctcctgctgtgccagacgcgtaactccaca



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 gaattcaggagcagcaggagcgctctaccctgacaagcaaaaccacagcctcggcgccacgacgacacctccagaacaaca  
 gttacagcatcaactacttctggtcagcaactaataagggatccattgtcaagatttggccactcatgtaaaaagcacagtacaa  
 aagcaaaagcattgccaatgggaagacggagcccagggaagaaactgaagcagaggatccctacaaagtacaggagctgattc  
 5 agatgcgcaaggagcagcgattggcagcgcttaaacgtatggcaatgataaatcgtcgcgaacggatgccactcccatatacg  
 gcgaagattgtcgcgaggtatatacagcgctgcatgcaggcgacccgatccctaaagcgtacacctggcagacgctgggatac  
 gccaaactgctgcactgccatggcgcatcggaacgggttgggtccctaaaccacttgcgaagagcttcgaggaaaggtgcgctgatc  
 taaagccagtgttggcaactttgtgatctacgttctctgttggcgccccggatccgtcgttatgtacaaaatctctatcgacgc  
 actggcagcacgaacaaaggattgaaaacattgtgcatcaggccctgcggcctaagctggcgttgctgcatccaatcatttcgga  
 10 aatgaccactaagttcccagatccgcgtctcatccaatacactgttgcaagttgcagaccatggatcgtttgtacgccagctaaa  
 gggttaacgggcatcgtgtactgatactcactcagatgaccaagatgttgatgttttggaaagcttttctcaactaccacggatcatattat  
 ctgctgttagatgggtctactcgggtggaacacggcagatccatgagcgggttaatggagataaacgaatcttctgtctc  
 ctctccacgcggctggttgagtggtggcatcaatttgacgggtgccgatactgtgatcttttactcactccgactggaacccacaatg  
 gatgcgcaggcccaagatcgttgccatcgtattgtcaaacgcgagatgtacatactaccgtctgtctccgaaagaacataga  
 15 gggttaacattcttaagaaggcaaaccaaaagcgaatgtgagcgacatggccatcgagggtggcaactttacaactacgtacttta  
 agagttccaccataaaggatctctttacaatggagcagagcagcaggacagtcgagccaagagaagtcggaaaacaaggat  
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 gacgagaacattcctattgcaacagaagatccaatgcggaaggaggtctcaagtgaactcagcaaggccgatctggagatg  
 20 cagaacttggttaaacagctctcaccgatagagcgatagccatgcgctttgtggaagaaactggagcagcatggacggcgga  
 caattgcgagccgagggaagcggagctggaggcccagaaacgcgagtgaggaggccaatcgcttggcgccatgcacaaggga  
 ggaggagctgttgaaagcaagaaacggaagcggaggagatgcttacctacagtcgcaaggattcagagtaacagggttaatac  
 aacagattccaattccaataagcgacgactggtgagggaataatcgcaaaactcagctcagaagctgagcaggagtgtagcag  
 ccatagcaccggtagcaacaacaagaacagtaaatcggaacacccgtggaataagccagaacagcctcaatcagactgtac  
 25 cagtggggtcagggaataagcagggtgaatagaacggggggggggtcagtagcagtagccgagggcaaaagtaacagcacga  
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 30 tggaagaagagctacaattgtctcctttaaacaatagtgatgatgaaagtaccaggatgaagaggagcagggaagagcagg  
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 tgggtgataattgatactgaagattcagaggcagatgtcaaatccagctccacctatggtacagcggcagatggttaagcccgaagaa  
 gccgaagcttgatggctgggtgacacgaccaggtgcaggacaccacaatgactagctccacctactacaatgtcagcga  
 35 ggaatcagacacggatgagcatcacgatagcaaggcggaggctaaagagccgccgcaaaattccgataagagcgacgagag  
 cgaggctgttgacacacaccacgtacaaggtcgcgcggcacagtaaaagatcaatctgtggaccctggacgtgagtcctcgtagc  
 aaacgcattgaataaaagcagcgccaataggagcctcaaaaaagcaccgaaggactgagtcacgccaagaggagctcagagc  
 gagccaaggcgaaagattactcagccaaagctgccgaagaagaagaactaacaacaaatctaacagaatattggcacctta  
 caccgctggatcgaagtccccccgagtaatgctcgtatccacacctgttacggcagcgagcgtagctcatcagcagcagtc  
 40 gtggtgtttcgggaggaaatgcctcctcagcgggaacagccaggtga

**Drosophila Gene Hit** TBLASTN with ORF2: brahma protein (M85049) and imitation-SWI protein (ISWI) (L27127) and chromodomain-helicase-DNA-binding (CHD-1)

45 **Human Homologue** BLASTX with EST TBLASTN with ORF2: Snf2-related CBP activator protein (SRCAP) (AF143946) and SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4 (SMARCA4) (NM\_003072.1)

	<b><i>Drosophila</i> EST</b>	several including SD07794 (AI534784), LD34465 (AA990657)
	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003453
5	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG9696 – domino an enzyme involved in DNA repair homology to snf2 family helicases
10	<b>Human homologue of Complete gene candidate</b>	CG9696- gi4557447 416409C913D6A935 [ref]NP_001261.1  chromodomain helicase DNA binding protein 1 [Homo sapiens] (1.90E-85
15	<b>Putative function</b>	snf2 helicase family member protein that contains a chromodomain, which occurs in proteins that are implicated in chromatin compaction, and an SNF2/SWI2-like helicase domain, which occurs in proteins 20 that are believed to activate transcription by counteracting the repressive effects of chromatin structure
25	<b>Confirmation by RNAi</b>	Loss of G1, peak, increase in G2M indicating arrest in G2/M

**Example 70 (Category 5)**

**Line ID** 99/31  
**Category** 2nd chromosome, small imaginal discs  
5 **Reversion** NR  
**Map Position** 53E

**Rescue ID** EcoR1

**Rescue Sequence 1**

10 AAGGCCCGACCAGAAACGAAATTTTCGGCGCGTNTTTTAAAATGCGCGGTAA  
ATTCACTTTGATTTTTGTTTTCTCTCTCGTTCTTCACACACACAGTTAGTTAGA  
TTGTGTGTTTCGCCTGGCTTTGCCTTTTAATTTTTTATTACCTGCATCCGATTTCG  
GTATTTGAAACAGCCGTTGAGTCTCCTTTGGCTTTTTTATCAGCGACGTCATCA  
GTGGCGGCAGAAGCAGAAGCGTCGACAGCGGCGGGGGATTTCGGCTGCATCTT  
15 TGGAGCCCCTTTCCGGCTGTGCCCCACGGCTTTCGCCACCCCCGCAGTAACC  
GATGCATTTTCCACATCGCTTACCTTATCGGCGGCATTTTCTTTGGCTGCCGTT  
TCTGCCGCTTTGTTAGCATCCTTTTCGTGCGGCGANGGCATGGAAAGATACAA  
ATCAGAATTGGATTACACTTGCTAATTTTTTGGCGGNCAATACAATGGTTCGG  
TGCGCCTATTCTTTTTTAATCGAATCGCAATTGAGTGTNAATTAAGTCTCCGCA  
20 ATGCAATTTGTGTATCTGTCTCCTCCCCGANC GAACAACGATNGAAAAAGGAA  
CCAGAAATAAAANAGGNAATGAAAAACACATTGCAATCTATAAGGCCACAC  
ACACACATATCATCCCGTCTACCANTCCATCGGATTCGANCCACANAANCCAT  
NTTTATACCNCAACGAACGNGGAAAAAACNATATCNGNAATTACCCCCCGAA  
AATTGTTGCCNCTTTTACCCAAATATTTACAACCNCCGTTCAATCACTCCTGGA  
25 ACATTCCNGGCTTTCCCAATTTTCNCCTTTACTACAATTTCAATGGTTTCTTTTT  
CCTCAC

**Rescue ID** BamH1

**Rescue Sequence 2**

30 CCTNAAATGTNGCGCTGGGNCCTAAANCGTCNCTCCTTGTGTCTCTCTTGTTTA  
CCGCGCTATGCTGATGTTGGCATGTGGTTCGATCCCCCTCCGTGTCGATGTTTA  
CAAAACCATNATTAGAGTTTGATGATTGAGTTCTCTTAACCTTTCCTTCCTCTT  
CCTTCCTTGGCTTTTGTTCATGCTAAATCCTTTAAATGGGGTTCTGCGTAGTTT  
AATGCCGAGGTACAGCAAACTTCAATATTCATGTTCCCTTGCCTCCCAAAC  
35 GAAATTAGCATTGGACGTCCCAAGGTTGAAGACATTTNATTATTTTAACATCT  
TTTNATTTTATTACATTTGAACTCTTACAAGTAATAATAATTACAATTAATAT  
TATAGCTGCAGCGGACAAAAAGGAGAAATCCCCCTCGCCGGTAATAAAGAAT  
CCAACAATAAGGATGCTNAAAANGAAGAAAACCCNAAAAAGGAGAAGAAAA  
ATCGGAANAAGGNGATGAGCCNGAAGATGAGGNNGATGAGAAAGCTAGCGA  
40 TGAAGAGAGCGAGAAGAAGAAANCGANATGAGATGCAGAGGACAGATAAAG  
GATGCCACNGATGAATCCAAGCCAAAATCGGGAGCCGATAAGCCCAAGAAAC  
TGAGCCCAAGGCCAAGAATGGCAAGGTGGNT

**Genomic hit, Accession No.** CSC:AC020063

45

**Associated ORF**

Genscan ORF1 predicted sequences >16:48:25|GENSCAN\_predicted\_peptide\_1/722\_aa  
MPSPEHKDANKAAETAAKENAADKVSVDENASVTAGVAKAVGAQPERGSKDA  
AESPAAVDASASAATDDVADKKAKGDSTAVSNTESDAAAADKKEKSPSPVIKKS  
NNKDAKKEDNSEKDEENSEDGDEPEDEADEKASDEESEKKKPKLDAEDKIKDAT  
5 DESKPKSGADKPKKPEPKAKNGKVAKEEDDDEEDEDDEDAEDDDGDENDGLDK  
NNEVAEDDENVVLAIEIDRINENINKTRVDGLQTLHAICFGAQGKNNVVKKNLRS  
FAGFEFAKDSAEYNKKLEAIKKVDNKGLRSICEILTLDRKGSKNETVLRVLKFLM  
EPDESLCLEQGDEEEEEEDAEDEDLDEDEEDPPSEEDKKRKSGKSSGGAGRGSARN  
STGRPRRATAGKKMSAYVDFSSDDSEQKVAVPKRRRNDDSESGSDYNPSANS  
10 SDGGRGGGAGAAGRKVPSRGGGRGPARKSRRRNSDSEEEEESEVSDADSDVPKR  
KRGSVGKRGRPAAPASAGRGRGRGAASRK RKDS DSEDEEVSEDEEEEDVSDFA  
SDQSEVCKFNLISSIWCFIKYMPIFQEERPKSKKPITPAKNSKANNKSKPAGKADS  
RSKKSKKESSEEDDDVDDKDESEDEPLTKKGKQAFPTDEQIRGYVKEILDKANL  
EITMKTVCQVYAKYPDFDLTDKKDFIKATVKADGVQDLGSPELIPRGRTT  
15 IWLICCCNNQIFGET

>16:48:25|GENSCAN\_predicted\_CDS\_1|2169\_bp  
atgccatcgccgcacgaaaaggtgctaacaagcggcgagaacgcgagccaagaagaatgccgccgataaggtgaagcgatg  
tgaaaaatgcatcgggttactgcgggggtggcgaaagccgtggggggcagccggaaaggggtctccaaagatgcagccgaatc  
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taaaaaaggaggacaactcggaaaaaggacgaggagaactcggaaagacggcgatgagccagaagatgaggctgatgagaagc  
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aaatcgggagccgataagcccaagaaacctgagcccaaggccaagaatggcaaggtggctaaggaggaggacgacgacga  
25 agaggacgaggatgatgaggatgccgaagatgacgatggagacgagaacgatggcctggacaagaacaacgaggtggccg  
aggatgatgagaatgtcgtcgtctcgcggagattgatcgcaatagagaataatcaacaagactcgtgtagatggtctgcaaacat  
tgcatgcaatctgcttggcgcccaaggcaagaacaatgtgtgcaagaagaactcgcgactcttggcggttcgagtttgccaagg  
attcagcggagtagacaacaaaaagctggaggccatcaaaaagggtggataataaggcgctgcgcagcatctgcgagatccttacc  
tcgatcgcaaggcgacgaagaacgagactgtcctcagtgctcgaatctctaaggaaccggacgagtcgcttggagca  
30 gggatgatgaggaggaggagaagatgccgaggacgaggatctggatgaagatgaggaggaccgccagtgaggaggaca  
agaagcgaagagcggaaaagtctagcggcgccgtggcagaggctctgcacgcaattccaccggacgtccaagggcgcgga  
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35 gaggaatcggaagttccgatgccgatagtgtgtcccaaacgttaacgtgttccgtgggtaaacgtggacgaccggcagct  
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40 gtcgatgacaaaagatgaatccgacgaggatgagccactaaccaaaaaggcgaacaggcattccaacggatgaacaaatacc  
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45 **Human Homologue** TBLASTN with ORF1: poor homology with DEK gene  
(D6S231E) (NM\_003472.1)  
**Drosophila EST** several including LD33301 (AA979048)



	<b>Annotated <i>Drosophila</i> genome genomic segment</b>	AE003805
	<b>Annotated <i>Drosophila</i> genome Complete gene candidate</b>	CG5935 - EG:EG0003.6 - novel with weak homology to DEK oncogene
5		CG8648 - EG:EG0003.3 - novel XPG/ flap endonuclease-like, DNA repair?
10	<b>Human homologue of Complete gene candidate</b>	CG5935- 1e-17 4503249 ref NP_003463.1 pD6S231E  DEK gene >gi 544150 sp P35659 DEK_H UMAN DEK PROTEIN >gi 284375
15		CG8648- 4758356 [ref NP_004102.1 pFEN1  flap structure-specific endonuclease 1;
20		MATURATION FACTOR 1 (MF1); DNase IV; RAD2_HUMAN(aa)
25	<b>Putative function</b>	CG5935: function unknown but putative DNA-binding protein predicted to be involved in chromosomal organisation. The translocation (6;9), associated with a specific subtype of acute myeloid leukemia, results in the fusion of two genes, dek and can, and the expression of a chimeric, leukemia-specific dek-can mRNA
30		CG8648: Novel XPG/ flap endonuclease-like, DNA repair protein
	<b>Confirmation by RNAi</b>	Both show slight reduction of G1 peak

REFERENCES

- Deak, P., Omar, M.M., Saunders, R.D.C., Pal, M., Komonyi, O., Szidonya, J., Maroy, P., Zhang, Y., Ashburner, M., Benos, P., Savakis, C., Siden-Kiamos, I., Louis, C., Bolshakov, V.N., Kafatos, F.C., Madueno, E., Modolell, J., Glover, D.M. (1997)
- 5 Correlating physical and cytogenetic maps in chromosomal region 86E-87F of *Drosophila melanogaster*. Genetics 147:1697-1722.
- Torok, T., Tick, G., Alvarado, M., Kiss, I. (1993) P-lacW insertional mutagenesis on the second chromosome of *Drosophila melanogaster*: isolation of lethals with different overgrowth phenotypes. Genetics 135(1):71-80
- 10 Saunders, R.D.C., Glover, D.M., Ashburner, M., Siden-Kiamos, I., Louis, C., Monastirioti, M., Savakis, C., Kafatos, F.C.(1989) PCR amplification of DNA microdissected from a single polytene chromosome band: a comparison with conventional microcloning. Nucleic Acids Res. 17:9027-9037
- Lefevre, G. (1976) A photographic representation and interpretation of the
- 15 polytene chromosomes of *Drosophila melanogaster* salivary glands. In: The Genetics and Biology of *Drosophila*, Eds Ashburner, M. and Novitski, E. Academic Press.
- Jowett, T. (1986) Preparation of nucleic acids. In "*Drosophila*: A Practical Approach." Ed Roberts, D.B. IRL Press Oxford.
- Pirrotta, V. (1986) Cloning *Drosophila* genes. In: . In "*Drosophila*: A Practical
- 20 Approach." Ed Roberts, D.B. IRL Press Oxford.
- Altschul, S.F. and Lipman, D. J. (1990) Protein database searches for multiple alignments. Proc. Natl. Acad. Sci. USA 87: 5509-5513

Burge, C. and Karlin, S. (1997) Prediction of complete gene structures in human genomic DNA. J. Mol. Biol. 268, 78-94.

Each of the applications and patents mentioned above, and each document cited or referenced in each of the foregoing applications and patents, including during the prosecution of each of the foregoing applications and patents ("application cited documents") and any manufacturer's instructions or catalogues for any products cited or mentioned in each of the foregoing applications and patents and in any of the application cited documents, are hereby incorporated herein by reference. Furthermore, all documents cited in this text, and all documents cited or referenced in documents cited in this text, and any manufacturer's instructions or catalogues for any products cited or mentioned in this text, are hereby incorporated herein by reference.

Various modifications and variations of the described methods and system of the invention will be apparent to those skilled in the art without departing from the scope and spirit of the invention. Although the invention has been described in connection with specific preferred embodiments, it should be understood that the invention as claimed should not be unduly limited to such specific embodiments. Indeed, various modifications of the described modes for carrying out the invention which are obvious to those skilled in molecular biology or related fields are intended to be within the scope of the following claims.

**CLAIMS**

1. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 70 or the complement thereof.
  - 5 (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 70, or a fragment thereof.
  - (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 70 or a fragment thereof.
  - 10 (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
2. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 1 to 14 or the complement thereof.
  - 15 (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 1 to 14, or a fragment thereof.
  - (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 1 to 14 or a fragment thereof.
  - 20 (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
3. A polynucleotide selected from:

- (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 15 to 19 or the complement thereof.
- (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 15 to 19, or a fragment thereof.
- 5 (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 15 to 19 or a fragment thereof.
- (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 10 4. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 20 to 30 or the complement thereof.
  - (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 20 to 30, or a fragment thereof.
  - 15 (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in Examples 20 to 30 or a fragment thereof.
  - (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 20 5. A polynucleotide selected from:
  - (a) polynucleotides comprising any one of the nucleotide sequences set out in Examples 31 to 53 or the complement thereof.
  - (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in Examples 31 to 53, or a fragment thereof.

- (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 31 to 53 or a fragment thereof.
- (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 5
6. A polynucleotide selected from:
- (a) polynucleotides comprising any one of the nucleotide sequences set out in 54 to 70 or the complement thereof.
- (b) polynucleotides comprising a nucleotide sequence capable of hybridising to the nucleotide sequences set out in 54 to 70, or a fragment thereof.
- 10
- (c) polynucleotides comprising a nucleotide sequence capable of hybridising to the complement of the nucleotide sequences set out in 54 to 70 or a fragment thereof.
- (d) polynucleotides comprising a polynucleotide sequence which is degenerate as a result of the genetic code to the polynucleotides defined in (a), (b) or (c).
- 15
7. A polynucleotide probe which comprises a fragment of at least 15 nucleotides of a polynucleotide according to any of Claims 1 to 6.
8. A polypeptide which comprises any one of the amino acid sequences set out in Examples 1 to 70 or in any of Examples 1 to 14, Examples 15 to 19, Examples 20 to 30, Examples 31 to 53 and Examples 54 to 70, or a homologue, variant, derivative or fragment thereof.
- 20
9. A polynucleotide encoding a polypeptide according to Claim 8.
10. A vector comprising a polynucleotide according to any of Claims 1 to 7 and 9.

11. An expression vector comprising a polynucleotide according to any of Claims 1 to 7 and 9 operably linked to a regulatory sequence capable of directing expression of said polynucleotide in a host cell.
12. An antibody capable of binding a polypeptide according to Claim 8.
- 5 13. A method for detecting the presence or absence of a polynucleotide according to any of Claims 1 to 7 and 9 in a biological sample which comprises:
- (a) bringing the biological sample containing DNA or RNA into contact with a probe according to Claim 9 under hybridising conditions; and
  - (b) detecting any duplex formed between the probe and nucleic acid in the  
10 sample.
14. A method for detecting a polypeptide according to Claim 8 present in a biological sample which comprises:
- (a) providing an antibody according to Claim 12;
  - (b) incubating a biological sample with said antibody under conditions which  
15 allow for the formation of an antibody-antigen complex; and
  - (c) determining whether antibody-antigen complex comprising said antibody is formed.
15. A polynucleotide according to according to any of Claims 1 to 7 and 9 for use in therapy.
- 20 16. A polypeptide according to Claim 8 for use in therapy.
17. An antibody according to Claim 12 for use in therapy.

18. A method of treating a tumour or a patient suffering from a proliferative disease comprising administering to a patient in need of treatment an effective amount of a polynucleotide according to any of Claims 1 to 7 and 9.
19. A method of treating a tumour or a patient suffering from a proliferative disease,  
5 comprising administering to a patient in need of treatment an effective amount of a polypeptide according to Claim 8.
20. A method of treating a tumour or a patient suffering from a proliferative disease, comprising administering to a patient in need of treatment an effective amount of an antibody according to Claim 12 to a patient.
- 10 21. Use of a polypeptide according to Claim 8 in a method of identifying a substance capable of affecting the function of the corresponding gene.
22. Use of a polypeptide according to Claim 8 in an assay for identifying a substance capable of inhibiting the cell division cycle.
- 15 23. Use as claimed in Claim 22, in which the substance is capable of inhibiting mitosis and/or meiosis.
24. A method for identifying a substance capable of binding to a polypeptide according to Claim 8, which method comprises incubating the polypeptide with a candidate substance under suitable conditions and determining whether the substance binds to the polypeptide.
- 20 25. A method for identifying a substance capable of modulating the function of a polypeptide according to Claim 8 or a polypeptide encoded by a polynucleotide according to any of Claims 1 to 7 and 9, the method comprising the steps of: incubating the polypeptide with a candidate substance and determining whether activity of the polypeptide is thereby modulated.



26. A substance identified by a method or assay according to any of Claims 21 to 25.
27. Use of a substance according to Claim 26 in a method of inhibiting the function of a polypeptide.
28. Use of a substance according to Claim 26 in a method of regulating a cell division  
5 cycle function.